



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 124854

TO: Manjunath N Rao
Location: REM-3B81/3C70
Art Unit: 1652
Friday, June 18, 2004

Case Serial Number: 10/038723

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Rao,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

THIS PAGE LEFT BLANK

From: Chan, Christina
Sent: Wednesday, June 16, 2004 5:28 PM
To: Rao, Manjunath N.; STIC-Biotech/CheMlib
Subject: RE: RUSH sequence search request for 10/038,723

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 & 1642
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Rao, Manjunath N.
Sent: Wednesday, June 16, 2004 10:51 AM
To: Chan, Christina
Subject: RUSH sequence search request for 10/038,723

Hello Christina,

Please authorize the request below as RUSH. The reason being , this is an amended case and due this bi-week.

Thanks
-Manjunath

From: Manjunath N. Rao
Art Unit 1652, Room 3B81
Mail Box in Room 3C70
Phone: 272-0939

Date: 6-16-04

Please search the following as soon as possible for application with serial number
10/038,723

1. SEQ ID NO: 2 and amino acids 1-295 against all commercial amino acid databases,
issued patents/published applications database and pending application

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

THIS PAGE LEFT BLANK

database. Please provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao
Art Unit 1652, Room 3B81,
Mail Box in Room 3C70,
Remsen Building, USPTO
400, Dulany St.
Alexandria, VA.
Phone: 571-272-0939

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 17, 2004, 17:43:18 ; Search time 20 Seconds

(without alignments)

Sequence: 1 MSFRSLIALSGLVCTGLANV.....SKTTATASKTSPTTRSGMSL 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Title: US-10-038-723-2
Perfect score: 2771
Sequence: 1 MSFRSLIALSGLVCTGLANV.....SKTTATASKTSPTTRSGMSL 534

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 Summaries

Database : PIR_78,*
1: pir1,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2771	100.0	534	2 A29776	glucan 1,4-alpha-glucosidase (EC 3.2.1.3) G2 precursor - Aspergillus awamori
2	2742	99.0	640	1 ALASGR	N;Alternate names: glucomylase G2
3	2742	99.0	640	2 A29166	C;Species: Aspergillus awamori
4	2620.5	94.6	639	2 J00607	C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 12-Jun-2003
5	2588.5	93.4	639	2 JT0479	R;Number: A93066; A29776
6	1935	69.8	612	2 JQ1346	A;Title: Molecular cloning and characterization of the glucoamylase gene of Aspergillus
7	1577	56.9	626	2 S36364	A;Reference number: A93066; MUID:85085934; PMID:6440004
8	1577	56.9	626	2 T49625	A;Accession: A93055
9	1497	54.0	493	2 JC6538	A;Molecule type: DNA
10	1321	47.0	616	2 S33908	A;Residues: 1-534 <NUN>
11	781.5	28.2	450	2 T39433	A;Cross-references: GB:K02465; PIDN:9454405; PIDN:AB59297.1; PID:9166505
12	724	26.1	604	1 JP0001	R;Number: A94514
13	676.5	24.4	519	1 A54549	Submitted to GenBank, February 1985
14	597	21.5	549	1 S48474	A;Reference number: A94514
15	522	18.8	778	1 ALBYG	A;Contents: annotation; revisions to the DNA sequence and coding regions for G2 form
16	522	18.8	767	1 JT0474	C;Comment: The DNA sequence was obtained from Genbank, release 55.0.
17	221.5	8.0	615	2 A64501	C;Superfamily: glucan 1,4-alpha-glucosidase homology <GAG>
18	181	6.5	1588	2 A66306	F;23-447/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
19	6.5	1588	2 H91188	Query Match 100.0%; Score 2771; DB 2; Length 534;	
20	172	6.2	622	2 G90250	Best Local Similarity 100.0%; Pred. No. 5.9e-179;
21	170.5	6.2	1275	2 T33369	Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
22	166.5	6.0	107	1 B60754	Db
23	5.8	1063	2 D86731	61 VVASSTDNDYFYWTRISGLVIKTLVDFRNGETSLSIYSTENIQAIVQGISNPSG 120	
24	5.8	888	2 T46726	Db	
25	5.7	1210	2 A25547	181 PLVRNDLSYVAQYNNQTGYDLWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240	
26	159	5.7	2271	2 F90073	Db
27	158	5.7	1283	2 T39174	121 DLSSGAGLGPKNEDTATGSGRPQRQGPBARTAMIGFGQMLDNGYSTATDW 180
28	5.7	1258	2 T39174	Db	
29	5.6	2232	2 T34434	121 DLSSGAGLGPKNEDTATGSGRPQRQGPBARTAMIGFGQMLDNGYSTATDW 180	

ice nucleation pro
ice nucleation pro
hypothetical serin
ice nucleation act
MS2 protein - yea
mann endo-1,4-beta
probable membrane
hypothetical prote
probable membrane
glucan 1,4 alpha g
hypothetical prote
aglutinin-like ad
endo-1,4 beta-xyla
hypothetical prote
ice nucleation pro

OY	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSTSYSTDAVKTPADGVSVIETHAASNG	420	OY	241 APILCIVMQSFWMGSFILANPFSRSRGCDANTLGSHTTFDPEAACDDSTFQCPSPALA	300
Db	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSTSYSTDAVKTPADGVSVIETHAASNG	420	Db	241 APILCIVQSFWMGSFILANPFSRSRGCDANTLGSHTTFDPEAACDDSTFQCPSPALA	300
OY	421 SMSBQYDSDGEQISARDLTWSAALTANNRNSVVAWSGETSASSVPGTCAATAIG	480	OY	301 NHKEVVDSPRSIYTLDGLSDSEAVAVYRYPEDTYNGNPWFCLTLAAEQJDALYQWD	360
Db	421 SMSBQYDSDGEQISARDLTWSAALTANNRNSVVAWSGETSASSVPGTCAATAIG	480	Db	301 NHKEVVDSPRSIYTLDGLSDSEAVAVYRYPEDTYNGNPWFCLTLAAEQJDALYQWD	360
OY	481 TYSSVTWTSWPSIVATGGTTATPTGSSVTSKTTASKSTKTRSGMSL	534	OY	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSTSYSTDAVKTPADGVSVIETHAASNG	420
Db	481 TYSSVTWTSWPSIVATGGTTATPTGSSVTSKTTASKSTKTRSGMSL	534	Db	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSTSYSTDAVKTPADGVSVIETHAASNG	420
RESULT 2					
A;Reference number: A90986; MUID:84261458; PMID:620865	A;Accession: A90986	A;Molecule type: DNA	A;Residues: 1-640 <BOE>	A;Cross-references: GB:X0712; GB:K02466; NID:92342; PIDN:CAA25303_1; PID:92343	A;Note: the authors translated the codon GAT for residue 317 as Asn
R.Svennson, B.; Larsen, K.; Gunnarsson, A.	Bur. J. Biochem. 154, 497-502, 1986	R.Nunberg, J.H.; Meade, J.H.; Cole, G.; Lawyer, P.C.; McCabe, P.; Schweickart, V.; Tal, F.	R.;Nunberg, J.H.; Meade, J.H.; Cole, G.; Lawyer, P.C.; McCabe, P.; Schweickart, V.; Tal, F.	A;Title: Characterization of a glucamylase G2 from <i>Aspergillus niger</i> .	A;Title: Molecular cloning and characterization of the glucamylase gene of <i>Aspergillus niger</i> .
A;Reference number: A91161; MUID:8616085; PMID:3081341	A;Contents: comparison of forms G1 and G2	A;Accession: A91161	A;Residues: 1-640 <NUC>	A;Cross-references: GB:K02465; NID:9454405; PIDN:AAB59296_1; PID:9166505	C;Comment: See also PIR:ALASGR.
A;Molecule type: protein	A;Comment: The large molecular form G1 is shown.	C;Comment: Smaller molecular forms of the enzyme, G2, arise by proteolytic cleavage(s) comparative towards soluble poly- and oligosaccharides.	C;Genetics:	C;Genetics: 72/1; 167/3; 200/1; 412/3	C;Genetics: 72/1; 167/3; 200/1; 398/3
C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase homology <GAG>	F;1-24/Domain: signal sequence #sttatus predicted <SIG>	F;1-24/Domain: signal sequence #sttatus predicted <SIG>	F;1-24/Domain: signal sequence #sttatus predicted <SIG>	F;1-24/Domain: signal sequence #sttatus predicted <SIG>	F;1-24/Domain: signal sequence #sttatus predicted <SIG>
C;Keywords: alternative splicing; extracellular protein; glycoprotein; glycosidase; hydrolytic enzymes; alternative splicing; extracellular protein; glycoprotein; glycosidase; hydrolytic enzymes	F;23-44/Domain: glucan 1,4-alpha-glucosidase G1 #sttatus experimental <GG1>	F;23-44/Domain: glucan 1,4-alpha-glucosidase G1 #sttatus experimental <GG1>	F;23-44/Domain: glucan 1,4-alpha-glucosidase G1 #sttatus experimental <GG1>	F;23-44/Domain: glucan 1,4-alpha-glucosidase G1 #sttatus experimental <GG1>	F;23-44/Domain: glucan 1,4-alpha-glucosidase G1 #sttatus experimental <GG1>
F;25-60/Product: glucan 1,4-alpha-glucosidase (Asn) (covalent) #sttatus experimental <GG2>	F;25-60/Product: glucan 1,4-alpha-glucosidase G2, short form #sttatus experimental <GG2>	F;25-60/Product: glucan 1,4-alpha-glucosidase G2, long form #sttatus experimental <GG2>	F;25-60/Product: glucan 1,4-alpha-glucosidase G2, short form #sttatus experimental <GG2>	F;25-60/Product: glucan 1,4-alpha-glucosidase G2, short form #sttatus experimental <GG2>	F;25-60/Product: glucan 1,4-alpha-glucosidase G2, short form #sttatus experimental <GG2>
F;195-649/Binding site: carbohydrate-binding site (Asn) (covalent) #sttatus experimental <GG3>	F;195-649/Binding site: carbohydrate-binding site: carbonyl group #sttatus experimental <GG3>	F;195-649/Binding site: carbohydrate-binding site: carbonyl group #sttatus experimental <GG3>	F;195-649/Binding site: carbohydrate-binding site: carbonyl group #sttatus experimental <GG3>	F;195-649/Binding site: carbohydrate-binding site: carbonyl group #sttatus experimental <GG3>	F;195-649/Binding site: carbohydrate-binding site: carbonyl group #sttatus experimental <GG3>
F;465-467,486,477,483,484,492,506,510,513,515,522,525,527,529,530,532/Binding site: carbohydrate-binding site	F;476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bi	F;476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bi	F;476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bi	F;476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bi	F;476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bi
Query Match					
OY	99.0%; Score 2142; DB 1; Length 640; Best Local Similarity 99.6%; Pred. No. 6-8e-17; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	OY	99.0%; Score 2742; DB 2; Length 640; Best Local Similarity 99.6%; Pred. No. 6-8e-17; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	OY	99.0%; Score 2742; DB 2; Length 640; Best Local Similarity 99.6%; Pred. No. 6-8e-17; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db	61 MSFRSLLAISGLVCTGLANVISKRATLSWLSNEATVARTAILNNIGADGAWNSGADGI	60	Db	1 MSFRSLLAISGLVCTGLANVISKRATLSWLSNEATVARTAILNNIGADGAWNSGADGI	60
OY	1 MSFRSLLAISGLVCTGLANVISKRATLSWLSNEATVARTAILNNIGADGAWNSGADGI	60	Db	1 MSFRSLLAISGLVCTGLANVISKRATLSWLSNEATVARTAILNNIGADGAWNSGADGI	60
Db	1 MSFRSLLAISGLVCTGLANVISKRATLSWLSNEATVARTAILNNIGADGAWNSGADGI	60	OY	61 VVASPSTNDPYTWRSGLVLUKLVLDFRNGDTSLISTENYSAQAIQGISMSG	120
OY	61 VVASPSTNDPYTWRSGLVLUKLVLDFRNGDTSLISTENYSAQAIQGISMSG	120	Db	61 VVASPSTNDPYTWRSGLVLUKLVLDFRNGDTSLISTENYSAQAIQGISMSG	120
Db	61 VVASPSTNDPYTWRSGLVLUKLVLDFRNGDTSLISTENYSAQAIQGISMSG	120	OY	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180
OY	61 VVASPSTNDPYTWRSGLVLUKLVLDFRNGDTSLISTENYSAQAIQGISMSG	120	Db	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180
Db	61 VVASPSTNDPYTWRSGLVLUKLVLDFRNGDTSLISTENYSAQAIQGISMSG	120	OY	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180
OY	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180	Db	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180
Db	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180	OY	121 DLSGAGLGEPKENDEAYTGSWRPQDGPAKRAMTAMIGFQWLNGYSTATIVW	180
OY	181 PLVRNDLSVVAQMNQIGDMLWEWNGSSPFTAVOHRAVEVSAPATVGSCSWCDQ	240	Db	181 PLVRNDLSVVAQMNQIGDMLWEWNGSSPFTAVOHRAVEVSAPATVGSCSWCDQ	240
Db	181 PLVRNDLSVVAQMNQIGDMLWEWNGSSPFTAVOHRAVEVSAPATVGSCSWCDQ	240	OY	301 NHKEVVDSPRSIYTLDGLSDSERAVAVRGPEDTYINGNPWFCLTLAAEQJDALYQWD	360
OY	301 NHKEVVDSPRSIYTLDGLSDSERAVAVRGPEDTYINGNPWFCLTLAAEQJDALYQWD	360	Db	301 NHKEVVDSPRSIYTLDGLSDSERAVAVRGPEDTYINGNPWFCLTLAAEQJDALYQWD	360

RESULT 4

JQ0607
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus sp.
N;Alternative names: glucoamylase
C;Species: Aspergillus sp.

G-Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Jun-2003
C;Accession: JQ0607
R;Shibuya, I.; Gomi, K.; Iimura, Y.; Takahashi, K.; Tamura, G.; Hara, S.
Agric. Biol. Chem. 54, 1905-1914, 1990
A;Title: Molecular cloning of the glucamylase gene of Aspergillus shirouسامي and its expression in Escherichia coli
A;Reference number: JQ0607; Muih:9112400; PMID:1136803
A;Accession: JQ0607
A;Molecule type: DNA
A;Residue: 1-639 <SHI>
A;Experimental source: strain RIB 2504
C;Comment: This enzyme catalyzes the release of glucose from the non-reducing ends of starch.
C;Genetics:
A;Introns: 72/1; 16/6/3; 199/1; 41/3
C;Superfamily: Glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase; hydrolyase; polysaccharide degradation
P;1-44/Domain: signal sequence #status predicted <SIG>
P;23-449/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
P;25-639/Domain: glucoamylase #status predicted <MAT>

Query Match 94.6%; Score 2620.5; DB 2; Length 639;
Best Local Similarity 94.3%; Pred. No. 1e-168;
Matches 500; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Db 1 MSFRSLLALSLGLVGLTGLANVISKRTAQLDWSLNSNATVARTAILNNIGADGAWSGADSGI 60
1 MSFRSLLALSLGLVGLVSKRTAQLDWSLNSNATVARTAILNNIGADGAWSGADSGI 60
61 VVASPSTONPDYFTWTDGLVLUKTLDLPRNGDTSLISTIENIISAOIIVGNSPNRG 120
61 VVASPSTONPDYFTWTDGLVLUKTLDLPRNGDTSLISTIENIISAOIIVGNSPNRG 120
61 VVASPSTONPDYFTWTDGLVLUKTLDLPRNGDTSLISTIENIISAOIIVGNSPNRG 120
121 DLSSGAGLGEPEKENDAYIGSWGRPQDGPAIATAMIGFGOMLLDNGYTSATDIW 180
121 DLSSG - GLGEPEKENDAYIGSWGRPQDGPAIATAMIGFGOMLLDNGYTSATDIW 179
181 PLVRNDISYVAQWNTQGYDLWEEVNGSFTIAVORHALVEGSAFATAVGSSCWSQDSQ 240
180 PLVRNDISYVAQWNTQGYDLWEEVNGSFTIAVORHALVEGSAFATAVGSSCWSQDSQ 239
241 ABEILCYQSEFWGSPFIANFDSSRSKDANTLIGSIHTDPDEAACDDSTPQCPSPRALA 300
240 ABEILCYQSEFWGSPFIANFDSSRSKDANTLIGSIHTDPDEAACDDSTPQCPSPRALA 299
301 NHKEVWDPSRSTYTLDGLSDSEAWAVGRYPEDTYINGNPWFCLTLAAEQLYDQMD 360
300 NHKEVWDPSRSTYTLDGLSDSEAWAVGRYPEDTYINGNPWFCLTLAAEQLYDQMD 359
361 KQGSLEVDVSLDFPKALYSDAATGTYSSSSTSSIVDAVKTAGFVSIYETHASNG 420
421 SMSEQYDKSDGEOLSDARDITWSYALLTANNRMSVVPASWGETSASSVPGTCATSAIG 480
420 SMSEQYDKSDGEOLSDARDITWSYALLTANNRMSVVPASWGETSASSVPGTCATSAIG 479
360 KQGSLEVDVSLDFPKALYSDAATGTYSSSSTSSIVDAVKTAGFVSIYETHASNG 420
Db 481 TWSVVTVSPSIVTGGTTATPTGGSVTSKTTATASKTTTRS 530
Db 481 TWSVVTVSPSIVTGGTTATPTGGSVTSKTTATASKTTTRS 530
Db 481 TWSVVTVSPSIVTGGTTATPTGGSVTSKTTATASKTTTRS 530

RESULT 5
 JTO479
 481 TTSVTTSWPSIVATGGTTATPTGGSVTSTSKTTASKSSTRS 530
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 480 TTSVTTWPSIVATGGTTATTGSGVTSTSKTTASKSSTTS 529

JTO479
 N:Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - *Aspergillus awamori*
 C:Species: *Aspergillus awamori*
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 02-Jun-2003
 C:Accession: JTO479
 R:Hayashida, S.; Kuroda, K.; Ohta, K.; Kuhara, S.; Fukuda, K.; Sakai, Y.
 Agric. Biol. Chem. 53, 923-929, 1989
 A:Title: Molecular cloning of the glucoamylase I gene of *Aspergillus awamori* var. kawachi
 A:Reference number: JTO479
 A:Accession: JTO479
 A:Molecule type: DNA
 A:Residues: 1-639 <HAY>
 A:Experimental source: var. kawachi
 C:Genetics:
 A:Gene: GAI
 A:Protein:
 A:Substrates: Glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase; glycosidase; hydrolase; polysaccharide degradation
 C:Superfamily: Glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase
 C:Keywords: glycosidase; hydrolysis; polysaccharide degradation
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:23-46/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F:25-639/Product: glucan 1,4-alpha-glucosidase #status predicted <MAT>
 F:494-538/Region: raw-starch-affinity region

glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus oryzae
 N;Alternate names: glucoamylase
 C;Species: Aspergillus oryzae
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 02-Jun-2003
 C;Accession: JQ1346
 R;Hata, Y.; Tsuchiya, K.; Kittamoto, K.; Gomi, K.; Kumagai, C.; Tamura, G.; Hara, S.
 Gene 108, 145-150, 1991
 A;Title: Nucleotide sequence and expression of the glucoamylase-encoding gene (glaa) from
 A;Reference number: JQ1346
 A;Accession: JQ1346
 A;Molecule type: DNA
 A;Residues: 1-612 <HAT>
 A;Cross-references: GB:D10698; DDBJ:D01108; NTID:gi160312; PID:BA01540.1; PID:gi160313
 A;Note: the authors translated the codon TTT for residue 213 as Tyr
 C;Comment: This enzyme hydrolyzes starch to glucose.
 C;Genetics:
 A;Gene: glaa
 A;Introns: 75/1; 169/3; 202/1; 414/3
 C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha
 C;Keywords: glycosidase; hydrolase; polysaccharide Degradation
 C;26-449/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 Query Match 69.8%; Score 1935; DB 2; Length 612;
 Best Local Similarity 70.3%; Pred. No. 1-4e-122;
 Matches 367; Conservative 59; Mismatches 90; Indels 6; Gaps 4;
 Qy 1 MSFRSLLALSGLVGLTGLA--NVIKSRAKTLDSWSNEATVARTAILNNAGDAWGWSGADS 58
 Qy 2 VSPFSSCLRALAIGLSSVLAQVOPVLRQATGLDTWLSTEAENFSRQALNNIGDOSAQAGASP 61
 Qy 59 GITVVASPSTDNPYIFTWTRDGLVLUKLVDLFRNGDTSLSLTENIQAQIVQGSNP 118
 Db 62 GUVIASPKSKSDPPYIFTWTRDGLVLUKLVDLFRNGDTSLSLTENIQAQIVQGSNP 121
 Qy 119 SGDLSGAGLGERPKFVNDEBTAYGSWGRFORDGPALARATAMICPGQWILDNGYTSATDI 178
 Db 122 SGAISSG_GLEGEKPNVETAAFTGAWGKFQDFGPALARATAMIFGEGEWENNTISIATDL 180
 Qy 179 VNPFLVRNDLSVVAQYQWNNGYDLEWEVNGSSEFTIAVGHRLAVYEGSAFATAVGSSCSNCD 238
 Db 181 VWPVVRNDLSVVAQYQWSQSGFDLWEVQOITSFTVAVSHRALVEGSSFAKTVGSSCPYCD 240
 Qy 239 SQPEELCYLQSTWGTGSTFLANDSSRSQKDANTILLGSIHTFPPEAACDDSTIQPCSPRA 298
 Db 241 SQPQRVCYLOSTWGTGSTFLANDSSRSQKDANTILLGSIHTFPPEAACDDSTIQPCSPRA 300
 Qy 299 LANHKEVWDSFRSIYTLDNLSPSEAVAVGVPYRBDTYTGNPNPFLCTLAABEOLYDALYO 358
 Db 301 LANHKEVWDSFRSIYAIINSGRAENQAVAVGVPYRBDTYTGNPNPFLCTLAABEOLYDALYO 360
 Qy 359 WDQKGSLLEVTDVSLDFKKALYSDAATGTYSSSSSTYSSLDVAKTFANGFVSTVETHAAS 418
 Db 361 WDKYKSLAITDVSLLPFKALYSSAATGTYASSTTVVKOIVSVAKYADGYVQTVOTYAS 420
 Qy 419 NGSMSEQWDKSDGEQLSARDLTYSAALLTANNRRNSVTPASNGETSASSVPGCAATSA 478
 Db 421 TGSMAEQTKTDQSQTSAARDLTYSAALLTANNRRNSVTPASNGETSASSVPGCAATSA 480
 Qy 479 IGYTSVVTWSWPSIVATVCGT-TTATPTGGSVTSKTT 518
 Db 481 SGTYSSVVTWSWPSIVATVCGT-TTATPTGGSVTSKTT 521

RESULT 7

S36364
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Neurospora crassa
 N;Alternate names: glucoamylase; glycoamylase
 C;Species: Neurospora crassa
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2003
 C;Accession: S36364; S13710; S13711; S25539
 R;Stone, P.J.; Makoff, A.J.; Parish, J.H.; Radford, A.
 Curr. Genet. 24, 205-211, 1993
 A;Title: Cloning and sequence analysis of the glucoamylase gene of *Neurospora crassa*.

A;Reference number: S36364; MUID:94037144; PMID:8221928
 A;Accession: S36364
 A;Molecule type: DNA
 A;Residues: 1-626 <STP>
 A;Cross-references: EMBL:X67291
 A;Koh-Laur, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Ainley, K.; Johann
 Enzyme Microb. Technol. 11, 692-695, 1989
 A;Title: Exported proteins of Neurospora crassa: 1-glucoamylase.
 A;Reference number: S13710
 A;Accession: S13710
 A;Molecule type: protein
 A;Residues: 36-'X', 62-'X', 64-65 <KOH>
 R;Koh-Laur, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Ainley, K.; Johann
 submitted to the Protein Sequence Database, January 1990
 A;Description: Exported proteins of Neurospora crassa 1: - glucoamylase.
 A;Reference number: S13711
 A;Accession: S13711
 A;Molecule type: protein
 A;Residues: 36-60, 'X', 62, 'X', 64-65 <KOW>
 C;Genetics:
 A;Gene: gla-1
 A;Introns: 82/2
 C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1
 C;Keywords: glycosidase; hydrolase; polyaccharide degradation
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-35/Domain: propeptide #status predicted <PRO>
 F;35-458/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F;36-626/Product: glucan 1,4-alpha-glucosidase #status experimental <MAT>
 Query Match 56.9%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 1.9e-98; Mismatches 130; Indels 10; Gaps 6;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;
 Qy 2 SPRSLILASLGGLVYCTGLANVISRATLDWSLSNEATVARTAILNNIGADGAWVGSGADSGIV 61
 13 AFOQAVLGLPDPDHEKRSDPIKE-SVDSVYIQTPIAQKNLICNIGASCGRASGAASGV 71
 Qy 62 VASPSTNDPYFYTWRDSDGLLTKLTLDFLRFG-DTSLSLSTENYISAQAIQODISNPSC 120
 72 VASPSSKSPDWWTWTBDALVTKLIVDEFTNDYNTLQNTQRYAAQAKLQKGSVSNPSG 131
 Db 121 DLSSGAGLGEPKFNVDLDTAYTGSWGRQFDGPAKARATAMIGFCQMLDNGYTSADIW 180
 132 SLSNAGAGLGEPKFMDLQDFGAWGRQFDGPAKRLAALIGFKWLVSNGYADTAKSIIW 191
 Qy 181 PLVRNDLSYVAQYWNOQYGDLMRVEVNGSSSPTFTAHOHRAVLVEGSAFATAVGSSCSWCDSO 240
 192 PIVKNDLAYTAQYWNNTGFDLWEEVNSSSFTTAIAHSHRLALVEGSAFAKSVGSSSCACDAI 251
 Db 241 APEIICYLQSFATGS-FILANEDSRSGKDANTLIGSHTEDPBAACDSTFOCCSPRAL 299
 252 APQICLFOQSFWSNSNGTYISNFVNRYSGKDINSVLTSHINFDPAGCDNTFOCSDRL 311
 Qy 300 ANHKEVVDSFRSIYTLINGLSDSEBAVAVGRYRPEDTYNGNPNWILCTLAABQLDALYQW 359
 312 ANHKVVUDSMR-FWGVNSGRTAGKAAGVRYAEDVYINGNPWLTAAEQLDYAVW 370
 Db 360 DKQGSLELVTDVSLDFKKALYSDAATGTYSSSSTYSSIVDAVKPFDAGEVSVTHEASN 419
 371 KKQGSTVTSTSLAFFKDLVPSVSTGTYSSSSSTYTAINAIVTYADGFVDIVAQYTPSD 430
 Qy 420 GSMSEQYDKSDGEQOLSAARDLITMSYALLTANRRNSVPAWMGETSASSVPGTCATSAI 479
 431 GSLAEQFDKDSGAPLSAHLTWSYASLARRAGIVPPWSGAAASNLPGCGSASTVA 490
 480 GTYSVYVTMSPVIVANGGTTT-AATPGSGS---VTSTSKTATASKT 524
 491 GSYATATAATSPANLTPTASTTVPPTQGCAADHEBLVTFNEKRTTSQQT 541

A;Residues: 30-106-138-151;68-181;217-223;260-294;310-316;321-334;336-342;369-415;423-4
 R;Jougioki, V.; Torkkeli, T.; submitted to the EMBL Data Library, August 1992
 A;Reference number: S31425
 A;Accession: S31425
 A;Molecule type: DNA
 A;Residues: 1-616 <JOU>
 A;Cross-references: EMBL:X68143; NID:92787; PIDN:CAM48243.1; PID:92788
 A;Residues: 30-53;72-89;145-154;217-223;260-294;423-426, 'X', 428-436 <FA3>
 A;Experimental source: strain ATCC 20495
 C;Genetics:
 A;Gene: gamP
 C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha
 C;Keywords: glycoprotein; glycosidase; hydrolase; poly saccharide degradation
 F1-29/Domain: signal sequence #status predicted <SIG>
 F27-49/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F30-616/Product: glucan 1,4-alpha-glucosidase #status experimental <MAT>
 F499,427/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F500,514,528,587/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match Best local Similarity 47.7%; Score 1321; DB 2; Length 616;
 Matches 257; Conservative 48.6%; Pred No. 3.2e-81; Mismatches 150; Indels 34; Gaps 6;
 Qy 14 CTGLANVIS-----KRALDLSWSNEATVARTAILNNIGADGAWNSGADSGIVVA 63
 Db 8 CAGAISLLCSLAIATAAPTELKARDLSSFIASERATIALOGALNNIGPDGSAVPGAGAGFWA 67
 Qy 64 SPSTDNPDPYTFWTRDGLVLUKTLVLFRNGDTSLSLSTENYISAQATVQGSLNSNPGD-L 122
 Db 68 SPSKANPDPYTFWTRDGLVLUKTLVLFRNGDTSLSLSTENYISAQATVQGSLNSNPGDLS 123
 Qy 123 SSGAGLGERPKPNVDETAYGSGWGRFORDSPALRATAMICPQWMLDNGYTSTANDIWPL 182
 Db 128 PDGVQGLGEPKFMVDFTRNGPFGPQRDGPAIRALMYSNWLIKNGPFAEAKTKWPI 187
 Qy 183 VRNDLSVYQWNGNTGTYDILWEENGSSFTIAYPHRALVEGSAFATAVGSSCSWCDSDQAP 242
 Db 188 IANDLSVYQWNGNQGFDLWEETVASSFFTONGHARALVEGAOLAHDLGVTCTGCD-QAP 246
 Qy 243 EILCULQSFVWFGSFLIANF--DSSRSKGKDANTLIGSIHTPPEACDDSTFQPSRALLA 300
 Db 247 EVLGCLQSFVWFGSFLIANF--DSSRSKGKDANTLIGSIHTPPEACDDSTFQPSRALLA 306
 Qy 301 NHKEVVDSEFRSIIYTLDGLDSSEAVALGVPEDTYGNPWFCLTLAAEBOQDLYQD 360
 Db 307 NFVKLTDTFRNLTYINAGIPEGQGVAVGRYKAEDYNGGPNWYLTTAABEFLIDRAQK 366
 Qy 361 KQGSLEVTDVSLDFEKKALYSDAATGTYSS--SSSYSSITDVAUKTFADGFVSVTHAAS 418
 Db 367 ARHVLTVDTSLSAFFDVTPEVTVREYKSGNANSPFAQIMDAVAYADSYVATEAKYIPS 426
 Qy 419 NGMSBQYDKDSGEQSARDLWISYAAUTTANNRRNSVUPASWGETSASSVPGTCATSA 478
 Db 427 NGSLSEQFNRTGTPLSAIDLWISYAAFTTMSQSRAGQPSWGSNSRNALPPPTCSAST 486
 Qy 479 IGTSSSVTVTWSWPSIVATGGTTTAMPSSGGSVUSTSKTTATASKTST 527
 Db 487 PGIV-----TPRAAGPARNVSSCQSVITFINATT 517

RESULT 12
 JP0001
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Rhizopus oryzae
 A;Name: 1,4-alpha-D-glucan glucohydrolase; glucoamylase
 C;Species: Rhizopus oryzae
 C;Date: 28-Dec-1987 #Sequence_revision 23-Aug-1996 #Text_change 16-Jun-2000
 C;Accession: JP0001
 R;Akbari, T.; Nakamura, N.; Tanaka, Y.; Kiuchi, N.; Shibano, Y.; Tanaka, T.; Amachi, T.
 Agric. Biol. Chem. 50, 957-964, 1986
 A;Title: Rhizopus raw-starch-degrading glucoamylase: its cloning and expression in yeast
 A;Reference number: A90022
 A;Accession: JP0001
 A;Molecule type: DNA
 A;Residues: 1-604 <ASH>
 A;Cross-references: GB:D00049; PIDN:BAA00033.1; PID:9218035
 A;Experimental source: strain SW0034
 A;Note: there are two errors in the published sequence (personal communication): GCT (116
 to the known amino acid sequence of 11 peptides from glucoamylase, including the amino-
 R;Tanaka, Y.; Akbari, T.; Nakamura, N.; Kiuchi, N.; Shibano, Y.; Amachi, T.; Yoshizumi,
 Agric. Biol. Chem. 50, 965-969, 1986
 A;Title: Comparison of amino acid sequences of three glucoamylases and their structure-fn

RESULT 11
 T39433
 Glucoamylase precursor - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #Text_change 12-Jun-2003

A; Reference number: A90023
A; Content: Rhizopus glucoamylase exists in multiple forms, Gluc 1, Gluc 2, and Gluc 3, and degrade raw starch.
C; Comment: Rhizopus glucoamylase homology; predicted secondary structure homology and domain
C; GeneID: 51/3;
C; Superfamily: Rhizopus glucan 1,4-alpha-glucosidase; glucan 1,4-alpha-glucosidase homolog
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 1-25 /Domain: signal sequence #status predicted <SIG>
F; 26-60 /Product: glucan 1,4-alpha-glucosidase (Gluc 1) #status predicted <GL1>
F; 34-18 /Domain: glucosidase; starch-binding domain homology <BD>
F; 116-604 /Product: (or 110-604) glucan 1,4-alpha-glucosidase (Gluc 3) #status predicted <GL3>
F; 159-604 /Product: glucan 1,4-alpha-glucosidase (Gluc 2) #status predicted <GL2>
F; 166-592 /Domain: glucan 1,4-alpha-glucosidase homology <GGG>

Query Match 26.1%; Score 724; DB 1; Length 604;
Best Local Similarity 36.8%; Pred. No. 5e-41; Index 42; Gaps 10;
Matches 165; Conservative 71; Mismatches 170; Indexes 42; Gaps 10;

QY	25 ATUOSWLNSBATVARTAILANIGAGAWGAGDSRIVVSPDNPYFTWTRSGVL 84
Db	168 STISSWIKKQEGISRFAMLRNINP ---PGSATOFIAASLSTAGPDYYFAWTDAALTS 222
Qy	85 KTLULFLR---NGTTSLSIENYISAQAVQGINSNPGCOLSGAGLGEKFNUDETAYT 141
Db	223 NVTIVEYNTLISGNKNTILNVTKDVTWPSVKQNSTSTVCN-----CLGEPKPNPBGSGT 276
Qy	142 GSWSGPQRQDGPALEATAMGFG-QWLDNGITSTADIWPLVRUDLSYKAQYMQQTGYD 200
Db	277 GANCRPQNQGPAEATTFIFADSLTQTKDASYTVGTILKPAIRFDQDLYVNNVNGCF 336
Qy	201 LWEEWNGSSPTTAVQHRAVEGAFATAVGSS- -CSWDSDOAPREILCYQSFWNGSFL 258
Db	337 LWEEWNGVHFYTLMKMRKGLLGADFAKRNGDSTRASTSSTASTANKISSFWNSNN 396
Qy	259 ANFBS-----SRSQGDANL---LGSHTPDPEAACDSTFOCSPRALNHKEVDS 308
Db	397 IONQSQVTTGQSKKQGKLLGADFAKRNGDSTRASTSSTASTANKISSFWNSNN 447
Qy	309 FRSTYTLNGGLSDBSAVAVGRYPEDTY-----YNQNPWFICLTLAAEQLDYALQWMDQG 363
Db	448 FASIVYPINKQNLPSLVGNISGRIYPTDTYNGNGNSQCNNSWELAVTGYAELYRAIKEWING 507
Qy	364 SLEYTDVSDFPKALYSDTAG-TYSSSSSTYSS1YDAVKTFAOGFVSTVETHAHSNGSM 422
Db	508 GVTVSSISLPPFKKRDSSATSGKKYTVGTSDFNNLAQNLIAADRFLSTVOLHANNGL 567
Qy	423 SEQDKSDGEQLSARLDLTSYAAITAN 450
Db	568 AEEFRDRTGCLSTGARDLTWSHASLTAS 595

RESULT 13

A54549 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast: (*Saccharomyces cerevisiae*)
N1 Alternative name: 1,4-alpha-D-glucan Glucohydrolyase; glucoamylase
C; Species: *Saccharomyces cerevisiae*
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Jun-2003
C; Accession: A54549; S14596
R; Hostinova, E.; Balanova, J.; Gasperik, J.
R; FEMS Microbiol. Lett. 67, 103-108, 1991.
A; Title: The nucleotide sequence of the glucoamylase gene GLA1 from *Saccharomyces cerevisiae*
A; Reference number: A54549; MUID:92137640; PMID:1840532
A; Accession: A54549
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-519 <HOS>
A; Experimental source: KZ
A; Note: Sequence inconsistent with nucleotide translation
A; Note: Sequence extracted from NCBI backbone (NCBInr:78827, NCBIProtein:78828)
R; Hostinova, E.; Gasperik, J.; submitted to the EMBL Data library, March 1991
A; Description: Nucleotide and deduced amino acid sequence of the glucoamylase gene from

A;Reference number: S14596
A;Accession: S14596
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271, 'T', 273-519 <H02>
A;Cross-references: EMBL:X58117
C;Genetics:
A;Gene: G1AL
C;Superfamily: glucan 1,4-alpha-glucosidase, yeast type; glucan 1,4-alpha-glucosidase hc
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;41-506/Domain: glucan 1,4-alpha-glucosidase homology <GAC>
Query Match 24.4%; Score: 676.5; DB 1; Length 519;
Best Local Similarity 36.1%; Pred. No. 6.4e-38; Mis.matches 176; Index 63; Gaps 16;
Matches 175; Conservative 71; Nt.matches 176; Indels 63; Gaps 16;
Qy 24 RATLISWLSNEATARTATLANNIGDGAWSGADSGIVVAVSPSTDNPYFTWTDSLGL- 82
Db 42 RTDIEFLFDKQDKDSILYLYLQNLAYPEGQENDGPGTVIASPTSSNPDTYQWTDSAIT 101
Qy 83 ---VIKTLVLFRLFRNGDTSLSLTIENYISAQAIYQGQISNPSG--DSSGAGLGEPKPNVE 137
Db 102 FLTVISELED--NNNTNTLAKAVEYINTSYNLTTSNPGSFSDDENHKLGEPKPNTDG 159
Qy 138 TAYFGWSGRPQRDGALRATAM-----IGGCQWL-----DNGYTSATDIPMLVR 184
Db 160 SAYVGAWGRPQNDGPPLRAVASYRVLYNDVNSLNKQLVLDGPDINFSI-EDIVKNI 218
Qy 185 NDJUSVVAQWNTQNTGQDLWREBNGSFPTIAVORHALVEGSAFATV-----GSSCSWCD 238
Db 219 PDLVIVIGWMDSTGQDLMWENQGRHLFFTSVQOKAL---AYAVDIKSDDGDAASYLD 274
Qy 239 SQAPEILCYLQSFWG-----SFLANED---SSRGKDANTLGSHTFPDPACDD 288
Db 275 STASLIESYLGSQDGFWNTDVHNIVENPDLLQONRSQGLDSATYTGPLLTHD-IGESS 333
Qy 289 STFOPCSPPRALANIKHEVWDSPRSIYTLDNGLSDSEAVAVORYPETY-----YNGNPWF 343
Db 334 TPFDUDNEVULQSYLTDNKKRYSVNSAY-SAGAAIGRYPPEVINGDGSSECNPWFL 391
Qy 344 CTLLAAEOLYDALQWMDKGQSLEYT--DVSLLDEFFKALYSDAAT-----GTYSSSS 391
Db 392 ATAYAQVQVKLVND-AKSAASNDITINKNYIDFKNKYIDLISTNGYSSSDSVTKSGS 450
Qy 392 STYSSIVDAVKTFAFGPVSVIETHMASGMSMQYDKSOGEQLSARDITWSYAALLTANN 451
Db 451 DEFNTVADNLVTFGDSFQVILDHINDDGSLNEQINRYTGYSTSAYSLTWSSGALLEAIR 510
Qy 452 RRNSV 456
Db 511 LRNKV 515

RESULT 14
S48474
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) SGAL - yeast (Saccharomyces cerevisiae)
N;Alternate names: glucoamylase; protein YIL099w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 02-Jun-2003
C;Accession: S48474; C26877; S27284
R;Bowman, S.; Churcher, C.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48455
A;Accession: S48474
A;Molecule type: DNA
A;Residues: 1-549 <BOW>
A;Cross-references: GB:247047; EMBL:238125; NID:9603997; PID:9763247; GSPDB:GN00009; MIP
R;Yamasita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STAL.
A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: C26817
A;Molecule type: DNA

A;Residues: 1-503, 507, 'W', '513-514, 'TG', '516 <YAM>
A;Cross-references: EMBL:MI6166; NID:GI72592; PIDN:AAA35042.1; PID:GI172593
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
REBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Saccharomyces cerevisiae
A;Reference number: S27284
A;Accession: S27284
A;Molecule type: DNA
A;Residues: 1-183, 'H', 185-190 <PAR>
A;Cross-references: EMBL:X13858; NID:94461; PIDN:CAA32071.1; PID:94463
C;Genetics: SGD:SGA1; MIPS:YIL039w
A;Gene position: 9L
A;Map position: 9L
A;Function:
A;Description: hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from the non-reducing end of branched chains of homopolysaccharides.
C;Superfamily: glucan 1,4-alpha-glucosidase, Yeast type; glucan 1,4-alpha-glucosidase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; yeast vacuole
F;77-536/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
Query Match 21.5%; Score 597; DB 1; Length 549;
Best Local Similarity 30.4%; Pred. No. 1-6e-32;
Matches 153; Conservative 89; Mismatches 202; Indels 60; Gaps 14;
Qy 1 MSFSSLALASGLVCGTGLANVISKRATDLSWLNRAVTATAIINNIGADGAWNSGADSGI 60
Db 56 VQLRDVVLNGTIVVWD-SNGAWDSALEEWLQGOKKVSIKIFENIGSAVYPS-ISPGV 113
Qy 61 WASPSTDOPDYFYTWTGTRSGVLUKTLDLFRNGDTSLISTENYISQAIVQOISNSG 120
Db 114 VIASPSTQTHPDYFQWIRDSLNTINSIVS--HSAGPAIETLUQYLNVSFHLLQRSSNN-- 167
Qy 121 DLSSGAG----LGEPKENUDETAYTGSWRGPORDGALLRATAMIGFGQQMLDNG-- 170
Db 168 TLGAGIGYIINDTVVALGDKPNKNDWRAFTEDWGRPQNDGPALARSTAALKIDYIKQSGLDL 227
Qy 171 ----YSTATDIWPLVRLDLSVVAQYWNQTGDIWEEYNGSSRFITIAVORHALVESSA 225
Db 228 GAKVPPFQSTA-DIFDDIVRDLRFIDHWNSSGFDLWEEVNGMHFPTLVLQLSAVDKSLS 286
Qy 226 FATAVGSSCSWC---SQAPELCIVL---QSWFTGFSFLANF-----DSSRGDA 270
Db 287 YFNASERSSPFVVELRQTRRDISKFVLDPANGFINGKY--NYIVGTPMIADTLRGIDI 343
Qy 271 NTLIGSISHTFPPEAACDDSTFQCPSPRALANKHEVKVDSFRSYIYTLDGJSDSEAVAVGRY 330
Db 344 STLLAANTVHDAPS-A-SHLFDFINDPAVNLTHMLHRSIVPINDSSKNGTIALGRY 402
Qy 331 PEDTY----YNGNPWFCLTAAABOLYDLYQMDKQGSLEVTDVSLDFPKALYSDAATG 385
Db 403 PEDVYDGYGFEGEGNPWVLATCTASTLYQLYRHSIEQDHLVPMNDNSNAFWSELVFS 462
Qy 386 TYSS-----SSTYSSIVDAVKTFADGIVSVIETHAASNQMSUEQVQKSDGQ 433
Db 463 NLTTLGNDEGYLILEBNTPAFNQTIQKIFOLADSFLVLUKKAHVGTDGELSEQFNQYTGFM 522
Qy 434 LSARDITLWSYALLTANNRRNSV 457
Db 523 QGAQHILTWSYTFMDAQVIRQEV 546

RESULT 15

ALB1G
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: 1,4-alpha-D-glucan Glucosidase; glucoamylase
C;Species: Saccharomyces cerevisiae
C;Accession: A21896; A23470
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 05-Sep-1997
R;Yamashita, I.; Suzuki, K.; Fukui, S.
J. Bacteriol. 161, 567-573, 1985
A;Title: Nucleotide sequence of the extracellular glucamylase gene STA1 in the yeast S. cerevisiae
A;Reference number: A21896; MID:85104778; PMID:3918017
A;Note: S. diastaticus

Search completed: June 17, 2004, 17:48:00

Job time : 22 sec

A;Accession: A21896
A;Molecule type: DNA
A;Residues: 1-178 <VAL>
A;Experimental source: strain S106-9A; ATCC 60709
R;Yamashita, I.; Suzuki, K.; Saluzzo, F.
Agric. Biol. Chem. 50, 475-482, 1986
A;Title: Proteolytic processing of glucoamylase in the yeast *Saccharomyces cerevisiae*.
A;Reference number: A23470
A;Contents: signal sequence cleavage site
A;accession: A23470
A;Molecule type: protein
A;Residues: 1-65 <YAZ>
C;Genetics:
A;Gene: STA1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase STA1; glucan 1,4-alpha-glucosidase homeologous genes
C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide catabolism; signal sequence #status experimental <SIG>
F;1-32/Domain: glucan 1,4-alpha-glucosidase #status predicted <MP>
F;33-778/Product: glucan 1,4-alpha-glucosidase homology <GAG>
F;6,319,333,425,434,445,54,55,61,731,752/Binding site: carbohydrate (Asn) (covalent)
F;635/Active site: Asp #status predicted

Query Match 18.8%; Score 522; DB 1; Length 778;
Best Local Similarity 30.5%; Pred. No. 2.9e-27;
Matches 139; Conservative 80; Mismatches 177; Indels 60; Gaps 15;
Qy 1 MSFSSLALASGLVCGTGLANVISKRATDLSWLNRAVTATAIINNIGADGAWNSGADSGI 60
Db 324 VQLRDVVLNGTIVVWD-SNGAWDSALEEWLQGOKKVSIKIFENIGSAVYPS-ILPGV 381
Qy 61 WASPSTQTHPDYFQWIRDSLNTINSIVS--HSAGPAIETLUQYLNVSFHLLQRSSNN-- 120
Qy 382 VIASPSTQTHPDYFQWIRDSLNTINSIVS--HSADPA-IETLUQYLNVSFHLLQRSSNN-- 435
Db 121 DLSSGAG----LGEPKENUDETAYTGSWRGPORDGALLRATAMIGFGQQMLDNG-- 170
Qy 121 DLSSGAG----LGEPKENUDETAYTGSWRGPORDGALLRATAMIGFGQQMLDNG-- 170
Db 436 TLGAGIGYIINDTVVALGDKPNKNDWRAFTEDWGRPQNDGPALARSTAALKIDYIKQSGLDL 495
Qy 171 ----YSTATDIWPLVRLDLSVVAQYWNQTGDIWEEYNGSSRFITIAVORHALVESSA 225
Db 496 GAKVPPFQSTA-DIFDDIVRDLRFIDHWNSSGFDLWEEVNGMHFPTLVLQLSAVDRSL 554
Db 226 FATAVGSSCSWC---SQAPELCIVL---QSWFTGFSFLANF-----DSSRGDA 270
Db 555 YFNASERSSPFVVELRQTRRDISKFVLDPANGFINGKY--NYIVGTPMIADTLRGIDI 611
Qy 271 NTLIGSISHTFPPEAACDDSTFQCPSPRALANKHEVKVDSFRSYIYTLDGJSDSEAVAVGRY 330
Db 612 STLLAANTVHDAPS-A-SHLFDFINDPAVNLTHMLHRSIVPINDSSKNGTIALGRY 670
Qy 331 PEDTY----YNGNPWFCLTAAABOLYDLYQMDKQGSLEVTDVSLDFPKALYSDAATG 385
Db 671 PEDVYDGYGFEGEGNPWVLATCTASTLYQLYRHSIEQDHLVPMNDNSNAFWSELVFS 730
Qy 386 TYSS-----SSTYSSIVDAVKTFADGIVSVIETHAASNQMSUEQVQKSDGQ 409
Db 731 NLTTLGNDEGYLILEBNTPAFNQTIQKIFOLADSFLVLUKKAHVGTDGELSEQFNQYTGFM 766

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2004, 17:35:48 ; Search time 59 Seconds
(without alignments)

2557.294 Million cell updates/sec

Title: US-10-038-723-2

Perfect score: 2771

Sequence: 1 MSFRSLIALSGLVCTGIANV.....SKTTATASAKTSTTRSGMSL 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:**

- 1: geneseqp1980s:**
- 2: geneseqp1990s:**
- 3: geneseqp2000s:**
- 4: geneseqp2001s:**
- 5: geneseqp2002s:**
- 6: geneseqp2003as:**
- 7: geneseqp2003bs:**
- 8: geneseqp2004s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2771	100.0	534 2	AAY18090 Truncated Aay18090 Aspergillus
2	2771	100.0	534 2	AAY23338 Aspergillus
3	2771	100.0	534 3	Aab03450 Aspergillus
4	2771	100.0	534 3	Aay7740 A. niger
5	2771	100.0	534 4	Aab48171 A. niger
6	2771	100.0	534 4	Aab61904 A. niger
7	2742	99.0	640 3	Aay7741 A. niger
8	2742	99.0	640 4	Aab61905 A. niger
9	2683.5	96.8	639 1	Aap40212 Sequence
10	2658	95.9	630 1	Aap81876 Sequence
11	2628	94.8	616 3	Aab15176 Aspergillus
12	2625	94.7	616 2	Aay5979 Aspergillus
13	2625	94.7	616 3	Aab15180 Aspergillus
14	2615	94.4	616 2	Aaw55976 Aspergillus
15	2615	94.4	616 3	Aab15178 Aspergillus
16	2614	94.3	616 3	Aab15184 Aspergillus
17	2612	94.3	616 3	Aab15181 Aspergillus
18	2612	94.3	616 3	Aab15182 Aspergillus
19	2604	94.0	616 2	Aaw55977 Aspergillus
20	2604	94.0	616 3	Aab15179 Aspergillus
21	2600.5	93.8	621 2	Aaw55978 Aspergillus
22	2589.5	93.5	621 3	Aab15183 Aspergillus
23	2584.5	93.3	621 3	Aab15182 Aspergillus
24	2523	91.1	1095 6	Abp96330 Alpha-amylase
25	2468	89.1	471 4	Abm00045 AMG SEQ I

ALIGNMENTS

26	1850.5	66.8	631 6	ABB80181 A. fumiga
27	1770	63.9	624 4	AAB48170 Thermascus
28	1689	51.4	581 5	AAY23339 Talaromyces
29	1674.5	60.4	591 2	AAY23337 Talaromyces
30	1615.5	58.3	630 5	Aam51596 Thielavia
31	1577	56.9	626 2	Aar71034 N. crassa
32	1425.5	51.4	581 3	AAB18823 Amino aci
33	1425.5	51.4	581 5	Aau79444 Fusarium
34	1425.5	51.4	581 7	Abp01925 Fusarium
35	1408.5	50.8	704 6	ABB80170 A. fumiga
36	1380.5	49.8	620 6	AAB80174 A. fumiga
37	1321	47.7	616 2	Aaw30155 Glucoamyl
38	725	26.2	579 6	Abp96332 Rhizopus
39	724	26.1	604 1	Aap60359 Glucoamyl
40	641.5	23.2	624 2	Aar77674 Glucoamyl
41	615.5	22.2	497 1	Aap70572 Glucoamyl
42	600.5	21.7	918 1	Aap60723 Sequence
43	374	29.3	1 Aap70183 Sequence	Aap70183 Sequence
44	181	6.5	1588 7	Adc01413 Enterohae
45	172	6.2	2 Aar22343 His(184)	Aar22343 His(184)

This sequence is a truncated A. niger glucoamylase G1 protein. The invention relates to a method of saccharifying a liquefied starch solution comprising: (a) a saccharification step during which one or more enzymatic bacttacharification stages (using a mutated Aspergillus niger Aaw55978 Aspergillus) take place; (b) one or more high temperature membrane separation steps; and (c) circulation of the saccharification enzyme, in which the membrane separation steps are carried out as an integral part of the saccharification step. The method can be used for the production of mono and/or oligosaccharides from starch, including

CC dextrose, trehalose, isomaltooligosaccharides, cyclodextrins or
CC maltooligosaccharides. The use of the membrane separation step improves
CC the efficiency of the process and improves yields and purity
XX Sequence 534 AA;

Query Match 100.0%; Score 2771; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.5e-214; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60
1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60

QY 61 VVASPSTNDPYFYTWTDSGLVLTKLVDLFRNGDTSLISTENYISQAIVOGISNPSG 120
61 VVASPSTNDPYFYTWTDSGLVLTKLVDLFRNGDTSLISTENYISQAIVOGISNPSG 120

Db 61 VVASPSTNDPYFYTWTDSGLVLTKLVDLFRNGDTSLISTENYISQAIVOGISNPSG 120
61 VVASPSTNDPYFYTWTDSGLVLTKLVDLFRNGDTSLISTENYISQAIVOGISNPSG 120

QY 121 DLSSGAGLGEPKFENDETATGSGWRPQDGPAKRTAMIGFCQWLDNGYSTATDWW 180
121 DLSSGAGLGEPKFENDETATGSGWRPQDGPAKRTAMIGFCQWLDNGYSTATDWW 180

Db 181 PLVRLNDLSTVAQMNQNTGDLWEENGSSFTIAVORHALVEGSAPATAVGSSCSWCDSQ 240
181 PLVRLNDLSTVAQMNQNTGDLWEENGSSFTIAVORHALVEGSAPATAVGSSCSWCDSQ 240

Db 241 APEILCYLQSFWTSFPIANFDSSRSKGDKANTLIGSIHTFPDEACDSTFQPCSPRALA 300
241 APEILCYLQSFWTSFPIANFDSSRSKGDKANTLIGSIHTFPDEACDSTFQPCSPRALA 300

QY 301 NHKEVUDSRSIYTINDGLSDSEAVAVGRPEPDITYNGNPWFCLAAEQYDALYQWD 360
301 NHKEVUDSRSIYTINDGLSDSEAVAVGRPEPDITYNGNPWFCLAAEQYDALYQWD 360

Db 361 KQGSLEVTVLSDPKALYSDAAGTGYSSSSTYSSIVDAVKITADGFSIVVETHAASNG 420
361 KQGSLEVTVLSDPKALYSDAAGTGYSSSSTYSSIVDAVKITADGFSIVVETHAASNG 420

QY 421 SMSBQYDSDGEQSLARDLTVSYAALLTANNRNSVVPASWGETSASSVPGTCATSAIG 480
421 SMSBQYDSDGEQSLARDLTVSYAALLTANNRNSVVPASWGETSASSVPGTCATSAIG 480

Db 481 TYSSVTWPSIVATGGTTATPTGSSVTSKTTASKSTTTRSGMSL 534
481 TYSSVTWPSIVATGGTTATPTGSSVTSKTTASKSTTTRSGMSL 534

RESULT 2

AAV23338 ID AAV23338 standard; protein; 534 AA.

AC AAY23338; XX

DT 02-SEP-1999 (First entry)

XX DE Aspergillus niger glucoamylase enzyme.

XX KW Glucoamylase enzyme; saccharification; starch hydrolygate;

KW dextrose syrup; syrup; ethanol; fuel; beverage; citric acid;

KW ascorbic acid; lysine; glutamic acid.

XX OS Aspergillus niger.

XX PN WO9928448-A1.

XX PD 10-JUN-1999.

XX PF 26-NOV-1998; 98WO-DK000520.

XX PR 26-NOV-1997; 97US-00979673.

PR 30-DEC-1997; 97DK-00001557.

PR 30-JUN-1998; 98US-0107657.

PR 10-JUL-1998; 98DK-00000925.

XX DR N-PSDB; AAX81797.

XX PT Nielsen BR, Nielsen RI, Lehmbbeck J;

XX DR WPI: 1999-404822/34.

XX PS Disclosure; Page 63-64; 79pp; English.

XX The present sequence represents a glucoamylase enzyme obtained from Aspergillus niger. The specification describes a Talaromyces emersonii glucoamylase enzyme. The glucoamylase enzymes have high thermal stability so that a saccharification process may be carried out within a shorter period of time or the processes may be carried out using a lower enzyme dosage. The glucoamylase enzymes can be used for saccharifying starch hydrolysate for converting starch or partially hydrolysed starch into a syrup containing dextrose. They can be used for producing organic compounds such as citric acid, ascorbic acid, lysine or glutamic acid.

SQ Sequence 534 AA;

Query Match 100.0%; Score 2771; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.5e-214; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60
1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60

QY 61 VVASPSTNDPYFYTWTDSGLVLTKLVDLFRNGDTSLISTENYISQAIVOGISNPSG 120
61 VVASPSTNDPYFYTWTDSGLVLTKLVDLFRNGDTSLISTENYISQAIVOGISNPSG 120

Db 121 DLSSGAGLGEPKFENDETATGSGWRPQDGPAKRTAMIGFCQWLDNGYSTATDWW 180
121 DLSSGAGLGEPKFENDETATGSGWRPQDGPAKRTAMIGFCQWLDNGYSTATDWW 180

Db 181 PLVRLNDLSTVAQMNQNTGDLWEENGSSFTIAVORHALVEGSAPATAVGSSCSWCDSQ 240
181 PLVRLNDLSTVAQMNQNTGDLWEENGSSFTIAVORHALVEGSAPATAVGSSCSWCDSQ 240

Db 241 APEILCYLQSFWTSFPIANFDSSRSKGDKANTLIGSIHTFPDEACDSTFQPCSPRALA 300
241 APEILCYLQSFWTSFPIANFDSSRSKGDKANTLIGSIHTFPDEACDSTFQPCSPRALA 300

QY 301 NHKEVUDSRSIYTINDGLSDSEAVAVGRPEPDITYNGNPWFCLAAEQYDALYQWD 360
301 NHKEVUDSRSIYTINDGLSDSEAVAVGRPEPDITYNGNPWFCLAAEQYDALYQWD 360

Db 361 KQGSLEVTVLSDPKALYSDAAGTGYSSSSTYSSIVDAVKITADGFSIVVETHAASNG 420
361 KQGSLEVTVLSDPKALYSDAAGTGYSSSSTYSSIVDAVKITADGFSIVVETHAASNG 420

QY 421 SMSBQYDSDGEQSLARDLTVSYAALLTANNRNSVVPASWGETSASSVPGTCATSAIG 480
421 SMSBQYDSDGEQSLARDLTVSYAALLTANNRNSVVPASWGETSASSVPGTCATSAIG 480

Db 481 TYSSVTWPSIVATGGTTATPTGSSVTSKTTASKSTTTRSGMSL 534
481 TYSSVTWPSIVATGGTTATPTGSSVTSKTTASKSTTTRSGMSL 534

DT 03-JAN-2001 (first entry)
 XX DE Aspergillus niger G2 glucoamylase.
 XX KW Glucoamylase G2; starch hydrolysis; high fructose corn syrup;
 KW thermal stability.
 XX OS Aspergillus niger.
 XX FH Key Peptide Location/Qualifiers
 FT 1. :27 /label= prepropeptide_sequence
 FT 27. :28 /label= tripeptidyl_amino_peptidase_cleavage_site
 FT 28. :534 /label= mature_glucoamylase
 FT XX WO20034452-A1.
 XX PD 15-JUN-2000.
 XX PR 07-DEC-1999; 99WO-DK000686.
 XX PR 07-DEC-1998; 98DK-00001616.
 XX PR 24-MAR-1999; 99DK-0000409.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PT Nielsen BR, Svendsen A, Bojsen K, Vind J, Pedersen H;
 PI DR WPI; 2000-43126/37.
 XX PT Variants of parent fungal glucoamylase useful for producing ethanol,
 PT beverages and in fermentation processes comprise a peptide extension at
 PT the amino terminal.
 XX PS Disclosure; Page 50-51; 61pp; English.
 XX CC The present sequence is the G2 glucoamylase from Aspergillus niger. It
 CC was used to construct a version of the enzyme which has improved thermal
 CC stability, and which can be used more efficiently in starch hydrolysis.
 CC This process is used during high fructose corn syrup production, as well
 CC as in the production of ethanol for fuel or beverage, and in fermentation
 CC processes for producing organic compounds such as citric acid, ascorbic
 CC acid, lysine and glutamic acid
 XX SQ Sequence 534 AA:

Query Match	100 %;	Score 2771;	DB 3;	Length 534;
Best Local Similarity	100.0 %;	Pred. No. 1.5e-214;		
Matches	534;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

XX OY 1 MSFRSIALSLASLIVCTGLANVSKRATLDWSWNEATVARTILINNAGDAWNSGADSGI 60
 Db 1 MSFRSIALSLASLIVCTGLANVSKRATLDWSWNEATVARTILINNAGDAWNSGADSGI 60
 OY 61 VVASPSTDNPQFYTWTRDSILSVLKTLVUDLFLRNGDTSLLSTENYISAQAVOGISNPSG 120
 Db 61 VVASPSTDNPQFYTWTRDSILSVLKTLVUDLFLRNGDTSLLSTENYISAQAVOGISNPSG 120
 OY 121 DLSGAGLGEKFENVDETAVGWSGRFQDGPALRATAMIGRGQWILDNGTSTATIDW 180
 Db 121 DLSGAGLGEKFENVDETAVGWSGRFQDGPALRATAMIGRGQWILDNGTSTATIDW 180
 OY 181 PLVRNDLSYVVAQWNGQTGYDIDWEEVNGSSFTIAVORALVEGSAFATAVQSSCWDQS 240
 Db 181 PLVRNDLSYVVAQWNGQTGYDIDWEEVNGSSFTIAVORALVEGSAFATAVQSSCWDQS 240
 OY 241 APEILCYLQSFMTGFSFLANFDSSRGKDANTLIGSHTPPEAEDDSTQPCSPRALA 300
 Db 241 APEILCYLQSFMTGFSFLANFDSSRGKDANTLIGSHTPPEAEDDSTQPCSPRALA 300
 OY 301 NHKEVUDSFRSIYTNDGLSSEAVAVGRYPTBDTYINGNPFLCTLAEEQVLYDALQMD 360

Db 301 NHKEVUDSFRSIYTNDGLSSEAVAVGRYPTBDTYINGNPFLCTLAEEQVLYDALQMD 360
 OY 361 KQGSLEVDLSDLFKKLYSDATGTYSSSSSTISSVDAVKTFADGVNSVTEHRSNG 420
 Db 361 KQGSLEVDLSDLFKKLYSDATGTYSSSSSTISSVDAVKTFADGVNSVTEHRSNG 420
 OY 421 SMSEQYDKSDGEOLSLARDTWSYAAUHTANNRRNSVVPASMGTSASVPGTCAATSAIG 480
 Db 421 SMSEQYDKSDGEOLSLARDTWSYAAUHTANNRRNSVVPASMGTSASVPGTCAATSAIG 480
 OY 481 TYSVVTSPSIVAGGTWTATPGSGSVTSTKTTAPASKSTTTRGMSL 534
 Db 481 TYSVVTSPSIVANGGTTATPGSGSVTSTKTTAPASKSTTTRGMSL 534

RESULT 4
 AAY77740
 ID AAY77740 Standard; protein; 534 AA.
 XX AC AAY77740;
 XX DT 22-MAY-2000 (first entry)
 XX DE A. niger G2 glucoamylase.
 XX KW Glucoamylase; variant; starch conversion; saccharification; ethanol;
 KW fuel; beverage; fermentation; citric acid; ascorbic acid; thermostable;
 KW glucoamylase; fungal.
 XX OS Aspergillus niger.
 XX PN WO20004136-A1.
 XX PD 27-JAN-2000.
 XX PR 09-JUL-1999; 99WO-DK000392.
 XX PR 15-JUL-1998; 98DK-00000937.
 XX PR 17-DEC-1998; 98DK-0001667.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PT Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
 PT Frandsen TP;
 XX DR WPI; 2000-182412/16.
 DR N-PSB; AAZ87542.
 XX PT Variant fungal glucoamylases with improved thermostability and increased
 PT specific activity, useful in saccharification processes.
 XX PS Claim 1; Page 78-81; 116pp; English.
 XX CC The invention relates to variant fungal glucoamylases comprising specific
 CC mutations. The variant comprises one or more mutation in position/region
 CC 1-18, 19-35, 40-62, 73-80, 93-127, 170-184, 200-212, 234-246, 287-319,
 CC 334-341, 353-374, 388-414, 445-470 of the parent G2 glucoamylase sequence
 (AAY77740) from A. niger, with the exception of N20C, A27C, S30P, Y48W,
 CC (AYY77740) from A. niger, with the exception of N20C, A27C, S30P, Y48W,
 CC Y50F, W52F, R54K/L, D55G, G57A, K108R, D112Y, Y116A/W, S119C/W/E/G/Y/P,
 CC W120H/L/F/Y, G121T/A, R122Y, P123G, Q124H, R125K, W170P, N171S, Q172N, CC
 CC T173G, G174C, Y175F, D176N/E, L177H/D, W178R/D, E179Q/D, E180D/Q,
 CC V181D/A/T, N182A/D, Y183H, S184H, W212F, R241K, A244C, D293E/O,
 CC A302Y, R305K, Y306F, D319N/E, Y312W, W317, E319D/Q, H319W, A319D, A319P,
 CC N319Q, G319S, B400Q/C, Q401E, G401P, E408P, L410F, S411A/G/C/H/D, and
 CC S460P. The glucoamylase variants are useful in a starch conversion
 CC process, especially continuous process which include a continuous
 CC saccharification process. The variants can be used for producing
 CC oligosaccharides, specialty syrups or ethanol for fuel or beverages.
 CC They can also be used in fermentation processes for producing organic
 CC compounds such as citric acid, ascorbic acid, lysine and glutamic acid.
 CC The glucoamylase variants have improved thermostability and/or increased
 CC specific activity. This is advantageous in industrial saccharification

CC processes. The risk of microbial contamination is also reduced when carrying the saccharification process at temperatures above 63 pluocC. An increased specific activity towards short chain saccharides such as CC maltose (without reducing the activity toward oligosaccharides) would also permit using a lower enzyme dosage and/or shorter process times. The CC present sequence represents the G2 glucoamylase from *A. niger*, the parent XX glucoamylase used for constructing the variants

SQ Sequence 534 AA:

Query	Match	100.0%; Score 2771; DB 3; Length 534;
Best Local Similarity	100.0%; Pred. No. 1.5e-214;	
Matches	534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGDAGAWNSGADSGI 60	
Db	1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGDAGAWNSGADSGI 60	
QY	61 VVASPSTDNPDYFTWTRDGLVLIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120	
Db	61 VVASPSTDNPDYFTWTRDGLVLIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120	
QY	121 DLSSGAGLGEPKENDEATYGSNRPQDGPALRATAMIGFQMLLDNGYSTATDIW 180	
Db	121 DLSSGAGLGEPKENDEATYGSNRPQDGPALRATAMIGFQMLLDNGYSTATDIW 180	
QY	181 PLVRNDLSVVAQYNNQTGDWLEEVNGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240	
Db	181 PLVRNDLSVVAQYNNQTGDWLEEVNGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240	
QY	241 APELICYQSFWTGSPFLANFDSSRSKGRANTLGSIHFTPEACDSTFQCPSPRALA 300	
Db	241 APELICYQSFWTGSPFLANFDSSRSKGRANTLGSIHFTPEACDSTFQCPSPRALA 300	
QY	301 NHKEVUDSRSIYTVDGLSDRAVAGRYPEDTYNGNPWFLCTLAEQYDALYQWD 360	
Db	301 NHKEVUDSRSIYTVDGLSDSEAVAGRYPEDTYNGNPWFLCTLAEQYDALYQWD 360	
QY	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSSSTSSIVDAVKTAADGFVSIVETHAASNG 420	
Db	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSSSTSSIVDAVKTAADGFVSIVETHAASNG 420	
QY	421 SMSEQYDKSDGEOLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480	
Db	421 SMSEQYDKSDGEOLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480	
QY	481 TYSVTWTSWPSIVATGGTTTAPTGGSSTVSTSKTATAKSITITRSGMSL 534	
Db	481 TYSVTWTSWPSIVATGGTTTAPTGGSSTVSTSKTATAKSITITRSGMSL 534	

RESULT 5

AAB48171	ID AAB48171 standard; protein; 534 AA.
XX	AC AAB48171;
XX	DT 02-APR-2001 (first entry)
DE	A. niger Glucoamylase polypeptide.
XX	KW Thermoascus crustaceus; glucoamylase; starch conversion; ethanol; KW maltose syrup; beverage; citric acid; ascorbic acid; detergent; KW thermostability; glucose; Glucoamylase.
OS Aspergillus niger.	
XX	FH Key location/Qualifiers
FH	1 .24 /note= "signal peptide"
FT	25 .534 /note= "mature protein"
FT	XX

PN WO200075296-A1.

XX 14-DEC-2000.

PD 02-JUN-2000; 2000WO-DK000301.

PF 02-JUN-1999; 99DK-00000779.

PR XX

PA (NOVO) NOVO NORDISK AS.

XX Nielsen BR, Kauppinen MS, Nielsen PI; DR WPI; 2001-071066/08. N-PSDB; AACB444.

XX Novel Thermascus crustaceus glucamylase polypeptide useful in a PT continuous starch conversion process, detergents and for producing PT oligosaccharides, specialty syrups, ethanol for fuel or drinking, and PT beverages.

XX Disclosure: Page 52-55; 61pp; English.

The invention provides a Thermascus crustaceus glucamylase polypeptide. CC The glucamylase is useful in a continuous starch conversion process, for CC producing oligosaccharides, specialty syrups such as maltose syrups, CC ethanol for fuel or drinking, ethanol, and organic compounds CC such as citric acid, ascorbic acid, lysine or glutamic acid. It is also CC useful in detergents such as laundry detergent compositions, dish wash compositions and/or hard surface cleaning compositions. The *T. crustaceus* CC glucamylase has higher thermostability than *Aspergillus niger* GI CC glucamylase. It also has higher specific activity and/or decreased CC glucose reversion tendency. The present sequence represents the *A. niger* CC GI glucamylase.

SQ Sequence 534 AA:

Query	Match	100.0%; Score 2771; DB 4; Length 534;
Best Local Similarity	100.0%; Pred. No. 1.5e-214;	
Matches	534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGDAGAWNSGADSGI 60	
Db	1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGDAGAWNSGADSGI 60	
QY	61 VVASPSTDNPDYFTWTRDGLVLIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120	
Db	61 VVASPSTDNPDYFTWTRDGLVLIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120	
QY	121 DLSSGAGLGEPKENDEATYGSNRPQDGPALRATAMIGFQMLLDNGYSTATDIW 180	
Db	121 DLSSGAGLGEPKENDEATYGSNRPQDGPALRATAMIGFQMLLDNGYSTATDIW 180	
QY	181 PLVRNDLSVVAQYNNQTGDWLEEVNGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240	
Db	181 PLVRNDLSVVAQYNNQTGDWLEEVNGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240	
QY	241 APELICYQSFWTGSPFLANFDSSRSKGRANTLGSIHFTPEACDSTFQCPSPRALA 300	
Db	241 APELICYQSFWTGSPFLANFDSSRSKGRANTLGSIHFTPEACDSTFQCPSPRALA 300	
QY	301 NHKEVUDSRSIYTVDGLSDSEAVAGRYPEDTYNGNPWFLCTLAEQYDALYQWD 360	
Db	301 NHKEVUDSRSIYTVDGLSDSEAVAGRYPEDTYNGNPWFLCTLAEQYDALYQWD 360	
QY	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSSSTSSIVDAVKTAADGFVSIVETHAASNG 420	
Db	361 KQGSLEVTDVSLDFPKALYSDAATGTYSSSSSTSSIVDAVKTAADGFVSIVETHAASNG 420	
QY	421 SMSEQYDKSDGEOLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480	
Db	421 SMSEQYDKSDGEOLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480	

QY 481 TYSVTWTSWPSIVATGGTTTATPGSGVSTSKTATASKTSTTRSGMSL 534
 Db 481 TYSSVTWTSWPSIVATGGTTTATPGSGVSTSKTATASKTSTTRSGMSL 534

RESULT 6

AAB61904
 ID AAB61904 standard; protein; 534 AA.
 XX
 AC AAB61904;
 XX
 DT 08-MAY-2001 (first entry)
 DE A. niger G2 glucoamylase.

KW Glucoamylase; variant; starch; dextrose; saccharification; maltodextrin; glucose syrup; fuel; ethanol; beverage; fermentation; citric acid; ascorbic acid.

XX Aspergillus niger.

OS

PH Key Location/Qualifiers

PT Peptide 1..24
 /note= "signal peptide"
 25..534 /note= "mature protein"

FT Protein
 XX WO20104273-A2.
 XX PD 18-JAN-2001.
 XX PP 07-JUL-2000; 2000WO-DK000373.
 XX PR 09-JUL-1999; 99DK-00000999.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
 PI Frandsen TP;
 XX DR WPI; 2001-138334/14.
 DR N-PSDB; AAC85099.

XX Novel variant of parent glucoamylase useful in starch conversion process, and for producing oligosaccharides, malodextrins, glucose syrups, fuel, drinking ethanol, beverage and organic compounds.

PS Claim 1; Page 51-53; 58pp; English.

XX The invention relates to a variant of a parent glucoamylase, comprising an alteration at positions 59, 66, 72, 119, 189, 223, 227, 313, 340, 342, 352, 379, 386, 393, 395, 402, 408, 416, 425, 427, 444, 486, 490, 494, where the alteration is independently an insertion, substitution or deletion of amino acid which occupies the position. The variant glucoamylase is useful for converting starch or partially hydrolyzed starch into a syrup containing dextrose, by saccharifying starch hydrolyzate. The variant is useful in the starch conversion process, for producing oligosaccharides, malodextrins or glucose syrups, fuel, drinking ethanol, beverage and in a fermentation process for producing organic compounds, such as citric acid, ascorbic acid, lysine and glutamic acid. It is useful for improving the thermal stability and/or specific activity of a parent glucoamylase. The present sequence represents an A. niger G2 glucoamylase, the parent enzyme from which the variant of the invention is derived

XX Sequence 534 AA;

Query Match 100.0%; Score 2771; DB 4; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1..5e-214; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFRSLIALSGLVCTIGLANVSKRATLDSWLSNEATVARTAIIINNIGADGAWVGADSGI 60
 Db 61 VVASPSTDNPYFYTWRDSCILKVLVLDLFRNGTISLSTENYISQAIVQGTSNPG 120
 Qy 61 VVASPSTDNPYFYTWRDSCILKVLVLDLFRNGTISLSTENYISQAIVQGTSNPG 120

Db 121 DLSSGAGLGERKENVDETAYGSGWGRQDOPALRATAMIOFGQWILDNGTSTATIDW 180
 Qy 121 DLSSGAGLGERKENVDETAYGSGWGRQDOPALRATAMIOFGQWILDNGTSTATIDW 180

Db 181 PLVRNDISYVQYQWNGTYDLEWEENGSSEFTIAVORHALVEGSAFATAVGSSCSWMSDQ 240
 Qy 181 PLVRNDISYVQYQWNGTYDLEWEENGSSEFTIAVORHALVEGSAFATAVGSSCSWMSDQ 240

Db 241 APEILCYLQSFWTGSPFLANFDSSRSKGKDANTLGSINTFDEPEAACDSDTFQPCSPRALA 300
 Qy 241 APEILCYLQSFWTGSPFLANFDSSRSKGKDANTLGSINTFDEPEAACDSDTFQPCSPRALA 300

Db 301 NHKEVUDSFRSYITLGLSDSEAVAVGR/PEDTYNGNPFLCTLAEGOLYDALYQWD 360
 Qy 301 NHKEVUDSFRSYITLGLSDSEAVAVGR/PEDTYNGNPFLCTLAEGOLYDALYQWD 360

Db 361 KQGSLEVTDVSLDFKKLYSDATGTYSSSSSTYSSIVDAVKTFAQDGPFVSVTETHASNG 420
 Qy 361 KQGSLEVTDVSLDFKKLYSDATGTYSSSSSTYSSIVDAVKTFAQDGPFVSVTETHASNG 420

Db 421 SMSEQTKDSERQSLSRDLTWSYAAITANRNRNSVUPASWGETSASSVSGCTCAATSIG 480
 Qy 421 SMSEQTKDSERQSLSRDLTWSYAAITANRNRNSVUPASWGETSASSVSGCTCAATSIG 480

Db 481 TYSVTWTSWPSIVATGGTTTATPGSGVSTSKTATASKTSTTRSGMSL 534
 Qy 481 TYSVTWTSWPSIVATGGTTTATPGSGVSTSKTATASKTSTTRSGMSL 534

Db 481 TYSSVTWTSWPSIVATGGTTTATPGSGVSTSKTATASKTSTTRSGMSL 534

RESULT 7

AY77741
 ID AY77741 standard; protein; 640 AA.
 XX AC AY77741;
 XX DT 22-MAY-2000 (first entry)
 XX A. niger G1 glucoamylase.

XX Glucoamylase; variant; starch conversion; saccharification; ethanol; fuel; beverage; fermentation; citric acid; ascorbic acid; thermostable; G1 Glucoamylase; fungal.

XX OS Aspergillus niger.

XX PN WO20004136-A1.

XX PD 27-JAN-2000.

XX PP 09-JUN-1999; 99WO-DK000392.

XX PR 15-JUL-1998; 98DK-00000937.

BR 17-DEC-1998; 98DK-00001667.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
 PI Frandsen TP;
 XX DR N-PSDB; AAC87843.

XX Variant fungal glucoamylases with improved thermostability and increased PT specific activity, useful in saccharification processes.

XX Disclosure; Page 91-93; 116pp; English.

QY 1 MSFRSLIALSGLVCTIGLANVSKRATLDSWLSNEATVARTAIIINNIGADGAWVGADSGI 60

CC The invention relates to variant fungal glucoamylases. The variants
 CC comprise specific mutations in the parent G2 glucoamylase (AMG) sequence
 CC (AAV7740) from *A. niger* (see AAV8742 for specific positions of the
 CC mutations). The glucoamylase variants are useful in a starch conversion
 CC process, especially continuous process which include a continuous
 CC saccharification process. The variants can be used for producing
 CC oligosaccharides, specialty syrups, or ethanol for fuel or beverages.
 CC They can also be used in fermentation processes for producing organic
 CC compounds such as citric acid, ascorbic acid, lysine and glutamic acid.
 CC The glucoamylase variants have improved thermostability and/or increased
 CC specific activity. This is advantageous in industrial saccharification
 CC processes. The risk of microbial contamination is also reduced when
 CC carrying the saccharification process at temperatures above 63 °C. An
 CC increased specific activity towards short chain saccharides such as
 CC maltose (without reducing the activity towards oligosaccharides) would
 CC also permit using a lower enzyme dosage and/or shorter process times. The
 CC present sequence represents the GI glucoamylase from *A. niger*

XX Sequence 640 AA;

Query Match 99.0%; Score 2742; DB 3; Length 640;
 Best Local Similarity 99.6%; Pred. No. 4.4e-212; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFRSILALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60

Db 1 MSFRSILALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60

Qy 61 WVASPTNDPYFWTRDGLVLUKTLDIFRNGDTSLISTENIYISAQIVQGINSNSG 120

Db 61 WVASPTNDPYFWTRDGLVLUKTLDIFRNGDTSLISTENIYISAQIVQGINSNSG 120

Qy 121 DLSSGAGLGEPKFNDETAVTGSWGRPDRGPALARATAMIGFGQWMLDNGYTSTATIW 180

Db 121 DLSSGAGLGEPKFNDETAVTGSWGRPDRGPALARATAMIGFGQWMLDNGYTSTATIW 180

Qy 181 PLVRNDLSVVAQYWNQTYGDNWEEENGSSFTIAVQHARALVEGSAFATAVGSSCSWCDSQ 240

Db 181 PLVRNDLSVVAQYWNQTYGDNWEEENGSSFTIAVQHARALVEGSAFATAVGSSCSWCDSQ 240

Qy 241 APEILCYLOSFRTWPSKGDANTLGSIHPDEACDSTFOPCSPRALA 300

Db 241 APEILCYLOSFRTWPSKGDANTLGSIHPDEACDSTFOPCSPRALA 300

Qy 301 NHKEVUDSFRSIYLTNDGLSDESEAIVAVGRYPEDTYINGNPWFCLAAEQLDALYQMD 360

Db 301 NHKEVUDSFRSIYLTNDGLSDESEAIVAVGRYPEDTYINGNPWFCLAAEQLDALYQMD 360

Qy 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTSYTSDAVKTFADGIVSVIETHASNG 420

Db 341 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTSYTSDAVKTFADGIVSVIETHASNG 420

Qy 421 SMSBQDKSUSQEQSLARDLWMSYALLTANRNRMSVWPAWGEASSSPGTCAATSAG 480

Db 421 SMSBQDKSUSQEQSLARDLWMSYALLTANRNRMSVWPAWGEASSSPGTCAATSAG 480

Qy 421 SMSEQDKSDQEBOALSARDLWMSYALLTANRNRMSVWPAWGEASSSPGTCAATSAG 480

Db 421 SMSEQDKSDQEBOALSARDLWMSYALLTANRNRMSVWPAWGEASSSPGTCAATSAG 480

Qy 481 TYSSTVTTSPIVATGGTTTATPGGSWTISKTTASKTSTS 530

Db 481 TYSSTVTTSPIVATGGTTTATPGGSWTISKTTASKTSTS 530

RESULT 8

AA61905 ID AAB61905 standard; protein; 640 AA.

AC AAB61905; XX

DT 08-MAY-2001 (first entry)

DE A. niger protein sequence Id No. 13.

XX Glucoamylase; variant; starch; dextrose; saccharification; maltodextrin;
 KW glucose syrup; fuel; ethanol; beverage; fermentation; citric acid;

KW ascorbic acid.

XX Aspergillus niger.

XX OS

XX

XX WO200104273-A2.

XX PD 18-JAN-2001.

XX PF 07-JUL-2000; 2000WO-DK000373.

XX PR 09-JUL-1999; 93DK-00000999.

XX PA (NOVO) NOVO NORDISK AS.

XX Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV,

XX Frandsen TP;

XX DR

XX WPI; 2001-138334/14.

Novel variant of parent glucoamylase useful in starch conversion process, PT and for producing oligosaccharides, maltodextrins, glucose syrups, fuel, PT drinking ethanol, beverage and organic compounds.

XX Disclosure; Page 57-58; 58pp; English.

The invention relates to a variant of a parent glucoamylase, comprising an alteration at positions 59, 66, 72, 119, 182, 223, 227, 313, 340, 342, 352, 379, 386, 393, 395, 412, 408, 416, 425, 427, 444, 486, 490, 494, where the alteration is independently an insertion, substitution or deletion of amino acid which occupies the position. The variant

CC glucoamylase is useful for converting starch or partially hydrolyzed starch into a syrup containing dextrose, by saccharifying starch hydrolyzate. The variant is useful in the starch conversion process, for producing oligosaccharides, maltodextrins or glucose syrups, fuel, drinking ethanol, beverage and in a fermentation process for producing organic compounds, such as citric acid, ascorbic acid, lysine and glutamic acid. It is useful for improving the thermal stability and/or specific activity of a parent glucoamylase

XX Sequence 640 AA;

Query Match 99.0%; Score 2742; DB 4; Length 640;
 Best Local Similarity 99.6%; Pred. No. 4.4e-212; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFRSILALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60

Db 1 MSFRSILALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWNSGADSGI 60

Qy 61 WVASPTNDPYFWTRDGLVLUKTLDIFRNGDTSLISTENIYISAQIVQGINSNSG 120

Db 61 WVASPTNDPYFWTRDGLVLUKTLDIFRNGDTSLISTENIYISAQIVQGINSNSG 120

Qy 121 DLSSGAGLGEPKFNDETAVTGSWGRPDRGPALARATAMIGFGQWMLDNGYTSTATIW 180

Db 121 DLSSGAGLGEPKFNDETAVTGSWGRPDRGPALARATAMIGFGQWMLDNGYTSTATIW 180

Qy 181 PLVRNDLSVVAQYWNQTYGDNWEEENGSSFTIAVQHARALVEGSAFATAVGSSCSWCDSQ 240

Db 181 PLVRNDLSVVAQYWNQTYGDNWEEENGSSFTIAVQHARALVEGSAFATAVGSSCSWCDSQ 240

Qy 241 APEILCYLOSFRTWPSKGDANTLGSIHPDEACDSTFOPCSPRALA 300

Db 241 APEILCYLOSFRTWPSKGDANTLGSIHPDEACDSTFOPCSPRALA 300

Qy 301 NHKEVUDSFRSIYLTNDGLSDESEAIVAVGRYPEDTYINGNPWFCLAAEQLDALYQMD 360

Db 301 NHKEVUDSFRSIYLTNDGLSDESEAIVAVGRYPEDTYINGNPWFCLAAEQLDALYQMD 360

Qy 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTSYTSDAVKTFADGIVSVIETHASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTSYTSDAVKTFADGIVSVIETHASNG 420

QY 421 SMSEQTDKSDEGQLSARDLTSYALITANNRNSVPAQGETSASSVPGTCAATSAIG 480
 Db 421 SMSEQDYSKDSDEGQLSARDLTSYALITANNRNSVPAQGETSASSVPGTCAATSAIG 480
 QY 481 TYSVTWSPSIVATGTTTATPGSGSVTSTSKitTATASKTISIStSS 530
 Db 481 TYSVTWSPSIVATGTTTATPGSGSVTSTSKitTATASKTISIStSS 530

RESULT 9

ID AAP40212 standard; protein: 639 AA.
 XX
 AC AAP40212;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-JAN-1992 (first entry)

Sequence encoded by A.awamori glucoamylase genomic region.

KW Starch hydrolysis; glucose.

OS Aspergillus awamori.

PN WO8402921-A.
 XX
 PD 02-AUG-1994.
 XX
 PF 26-JAN-1984; 84WO-US000122.
 XX
 PR 28-JAN-1983; 83US-00463920.
 PR 20-DEC-1983; 83US-00563941.
 PR 27-APR-1987; 87US-00047552.

PA (CETU) CETUS CORP.
 XX
 PI Nurnberg JH, Flatgaard JE, Innis MA, Gelfand DH, Meade JH;
 XX
 DR WPI; 1984-201413/32.

XX DNA sequence coding for fungal glucoamylase protein - for expression in yeast etc. for prodn. of the enzyme.

XX Example; Table 1, Page 21-25; 66pp; English.

The inventors claim a modified DNA sequence coding for fungal glucoamylase protein or its single or multiple base substitutions derived from insertions or inversions is new (see AN40165). It is derived from natural, synthetic or semisynthetic sources and is capable, when correctly combined with a cleaved expression vector, of expressing a non-native protein having glucoamylase activity on transformation of a host organism by the vector. (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 639 AA:

Query Match 96.8%; Score 2683.5; -DB 1; Length 639;
 Best Local Similarity 98.1%; Preq. No. 2.3e-207;
 Matches 520; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSFRSLALSLSCVLTGLANVSKRATLDSWISNEATARTAIIINNGADGAWNSGADSGI 60
 Db 1 MSFRSLALSLSCVLTGLANVSKRATLDSWISNEATARTAIIINNGADGAWNSGADSGI 60

QY 61 YVASPSTDNPYFYTMRDSLQVLUVLDLRNGDTSLSLSTENYISAQIVQGSNSPQ 120
 Db 61 YVASPSTDNPYFYTMRDSLQVLUVLDLRNGDTSLSLSTENYISAQIVQGSNSPQ 120

QY 121 DLSSGAGLGERKFNVDTAYTGSWGRQRDGFALRATAMIGFGQWILDNGTSTADIV 180
 Db 121 DLSSG-GIGEPKFNVDTAYTGSWGRQRDGFALRATAMIGFGQWILDNGTSTADIV 179

RESULT 10

ID AAP81876 standard; protein: 630 AA.
 XX
 AC AAP81876;
 XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 15-MAR-1992 (first entry)

DB Sequence of amyloglucosidase.

XX Enzyme; brewing; bread-making; dextrin.

OS Aspergillus niger; NCI 22343.
 XX
 PN BP260160-A.
 XX
 PD 16-MAR-1988.
 XX
 PP 10-JUN-1987; 87EP-00401300.
 XX
 PR 10-JUN-1986; 86FR-00008387.
 PR 13-APR-1987; 87FR-00005207.
 PR 13-APR-1987; 87FR-00005208.

PA (TRGE) TRANSGENE SA.
 XX
 PI Labat N, Loison G, Lemoine Y;
 XX
 DR WPI; 1988-072593/11.
 DR N-PSDE; AN82019.

XX New DNA block for expressing amyloglucosidase in yeast - contg. gene plus transcription and export sequences, and transformed cells useful in brewing and bread making.

XX Example; Fig 2; 38pp; French.

CC ECORI-Sal I fragments of Aspergillus niger NCI 22343 were cloned in PCR22 and two clones contg. portions of the gene isolated using a pool of three probes-TG82, TG283, TG84- (AN82014-6) designed on the basis of already published SOs. The clones were designated pTG130 and 1831. A cDNA bank of A. niger NCI 22343 was screened for amyloglucosidase using probe TG33 (AN82017) which corresponded to AAS 163-172 of the mature protein (see AN82019). Oligo TG87 (AN82018) was used to confirm the identity of the clones detected. (Updated on 25-MAR-2003 to correct PR

QY .181 PLVRNDISYQVQYNNQTYDLYWEENGGSSFTIAVORHALVEGSAFATAVGSSCSWCDQ 240
 Db 180 PLVRNDISYQVQYNNQTYDLYWEENGGSSFTIAVORHALVEGSAFATAVGSSCSWCDQ 239

QY 241 APICLVLQSWTGSPFLANPDSSGKDANTLGSIHTEPEACDDSFQPCSPRLA 300
 Db 240 APICLVLQSWTGSPFLANPDSSGKDANTLGSIHTEPEACDDSFQPCSPRLA 299

QY 301 NHKEVWDSFRSYTTLNDGLSDSEAVAVGRAPEDTYIGNPMPLCTLAABOLYDALYQWD 360
 Db 300 NHKEVWDSFRSYTTLNDGLSDSEAVAVGRAPEDTYIGNPMPLCTLAABOLYDALYQWD 359

QY 361 KQSLTVTDLDFFKALYSDATGSSSSSTSYISIVDAVKTADGFVSIVETHASNG 420
 Db 360 KQSLTVTDLDFFKALYSDATGSSSSSTSYISIVDAVKTADGFVSIVETHASNG 419

QY 421 SMSEQTDKSDEGQLSARDLTSYALITANNRNSVPAQGETSASSVPGTCAATSAIG 480
 Db 420 SMSEQTDKSDEGQLSARDLTSYALITANNRNSVPAQGETSASSVPGTCAATSAIG 479

QY 481 TYSVTWSPSIVATGTTTATPGSGSVTSTSKitTATASKTISIStSS 530
 Db 480 TYSVTWSPSIVATGTTTATPGSGSVTSTSKitTATASKTISIStSS 529

CC field.) (updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardize OS field)

XX SQ Sequence 630 AA;

Best Local Similarity 95.9%; Score 2658; DB 1; Length 630; Matches 515; Conservative 2; Mismatches 3; Indels 10; Gaps 1;

Query Match 95.9%; Score 2658; DB 1; Length 630; Matches 515; Conservative 2; Mismatches 3; Indels 10; Gaps 1;

QY 1 MSFRSLLAISGLVCTGLANVSKRATLDSWLNRAVTARTALINNIGADGAWNSGADSI 60
1 MSFRSLLAISGLVCTGLANVSKRATLDSWLNRAVTARTALINNIGADGAWNSGADSI 60

Db 61 WVASPTDNPDIFYWTRDGLVLUKLVLDFRNGLWSLUSTIENYISAGAVOCISNPG 120
61 WVASPTDNPDIFYWTRDGLVLUKLVLDFRNGLWSLUSTIENYISAGAVOCISNPG 120

QY 121 DLSGGAGLGEPKFNUDETAVGSMQRQDGPALRATAMIGFGQMLLDNGYSTADIW 180
121 DLSSGAGLGEPKFNUDETAVGSMQRQDGPALRATAMIGFGQMLLDNGYSTADIW 180

Db 181 PLVRNDLSTVVAQYNNOTGIDLWEEVNGSSPFTIAVORHALVEGSAFATAVGSSWCDQ 240
181 PLVRNDLSTVVAQYNNOTGIDLWEEVNGSSPFTIAVORHALVEGSAFATAVGSSWCDQ 240

Db 171 PLVRNDLSTVVAQYNNOTGIDLWEEVNGSSPFTIAVORHALVEGSAFATAVGSSWCDQ 230

QY 241 APEILCYLOSFWTGSPILANFDSSRSKGDKANTULGSIHFPDEACDSTFQCPSPRALA 300
241 APEILCYLOSFWTGSPILANFDSSRSKGDKANTULGSIHFPDEACDSTFQCPSPRALA 300

Db 231 APEILCYLOSFWTGSPILANFDSSRSKGDKANTULGSIHFPDEACDSTFQCPSPRALA 290

QY 301 NHKEVWDSEFSRISIYTANDGSDSEAIVAVGRYPEDTYINGNPWFCLTAAEQLYQMD 360
301 NHKEVWDSEFSRISIYTANDGSDSEAIVAVGRYPEDTYINGNPWFCLTAAEQLYQMD 360

Db 291 NHKEVWDSEFSRISIYTANDGSDSEAIVAVGRYPEDTYINGNPWFCLTAAEQLYQMD 350

QY 361 KQGSLEVTDVSLDFKALYSDAATCTYSSSSSTSVIVAKTKPADGEVSIVETHAASNG 420
361 KQGSLEVTDVSLDFKALYSDAATCTYSSSSSTSVIVAKTKPADGEVSIVETHAASNG 420

Db 351 KQGSLEVTDVSLDFKALYSDAATCTYSSSSSTSVIVAKTKPADGEVSIVETHAASNG 410

QY 421 SMSROYDKSDGEQLSARDLTWSYALLTANNRNSWPASWGETSASSVPGTCAATSG 480
421 SMSROYDKSDGEQLSARDLTWSYALLTANNRNSWPASWGETSASSVPGTCAATSG 480

Db 411 SMSEODYKDSIDGEQSARDLTWSYALLTANNRNSWPASWGETSASSVPGTCAATSG 470

QY 481 TYSSTVTWSRIVAGGTITATPTGGSVTSKTTASKTSTTRS 530
481 TYSSTVTWSRIVAGGTITATPTGGSVTSKTTASKTSTTRS 530

Db 471 TYSSVTVTWSRIVAGGTITATPTGGSVTSKTTASKTSTSS 520

RESULT 11

AAI15176 ID AAI15176 Standard; protein; 616 AA.

AC AAI15176;

XX DT 11-DEC-2000 (first entry)

XX DE Aspergillus awamori glucoamylase.

XX KW Glucoamylase; enzyme; carbohydrase; glucose;

XX KW 1,4-alpha-D-glucan glucohydrolase.

OS Aspergillus awamori.

XX PN WO200043504-A1.

XX PD 27-JUL-2000.

XX PR 10-JAN-2000; 2000WO-US000532.

XX PR 22-JAN-1999; 99US-00236063.

XX PA (IOWA) UNIV IOWA STATE RES FOUND INC.

XX PI Allen MJ, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R; Ford C;

XX DR WPI: 2000-514725/46.

XX PT Fungal glucoamylase for selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose, has mutation pair Asn20Cys coupled with Ala27Cys forming disulfide bond, between the two stabilizing members.

XX PS Disclosure; Page 152-153; 160pp; English.

XX The present sequence is glucoamylase (1,4-alpha-D-glucan glucohydrolase; B.C. 3.2.1.3). This enzyme is a carbohydrate, and cleaves D-glucose from the nonreducing ends of maltotrioligosaccharides, attacking alpha-(1,4)-, alpha-(1,6)-, and alpha-(1,6)-glucosidic bonds. The present invention relates to mutant glucoamylases (see AAI15176-B15184), which have increased thermostability, increased pH optimum and reduced isomaltose formation. The mutant proteins are useful for the selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose

XX SQ Sequence 616 AA;

Query Match 94.8%; Score 2628; DB 3; Length 616; Best Local Similarity 99.6%; Pred. No. 6..5e-203; Matches 504; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 25 ATUDSWLNRAVTARTALINNIGADGAWNSGADSGIVASPVSPDNPDIFYWTRDGLV 84

Db 1 ATUDSWLNRAVTARTALINNIGADGAWNSGADSGIVASPVSPDNPDIFYWTRDGLV 60

QY 85 KTIVDLPFNGDTSLSTIENYISAOATVQGISNPQDGSQDSSGAGLGEPKFNUDETAVG 144

Db 61 KTIVDLPFNGDTSLSTIENYISAOATVQGISNPQDGSQDSSGAGLGEPKFNUDETAVG 120

QY 145 GRPORDGPALRATAMIGFGQMLLDNGYSTADIWPLVPLVRNDLSTVVAQYNNOTG 180

Db 121 GRPORDGPALRATAMIGFGQMLLDNGYSTADIWPLVPLVRNDLSTVVAQYNNOTG 180

QY 205 VNGSSPFITAVORHALVEGSAFATAVGSSCSWCDQSARBLICLQSFRTGSPFLAN 264

Db 181 VNGSSPFITAVORHALVEGSAFATAVGSSCSWCDQSARBLICLQSFRTGSPFLAN 240

QY 265 RSGKDANTULGSIHFPDEACDSTFQCPSPRALAQNKEVWDFSPRSYTLGLSPSE 324

Db 241 RSGKDANTULGSIHFPDEACDSTFQCPSPRALAQNKEVWDFSPRSYTLGLSPSE 300

QY 325 VAVGRYPEDTYINGNPWFCLTAAEQLYQMDYQDOKGSLEVTDVSLDFPKALYSD 384

Db 301 VAVGRYPEDTYINGNPWFCLTAAEQLYQMDYQDOKGSLEVTDVSLDFPKALYSD 360

QY 385 GTISSSSSTVSSIVDAVTKPADGEVSIVETHAASNGSNSSEQYKQDSGQLSARDLT 444

Db 361 GTISSSSSTVSSIVDAVTKPADGEVSIVETHAASNGSNSSEQYKQDSGQLSARDLT 420

QY 445 ALLTANNRNSWPASWGETSASSVPGTCAATSGTSSVTVTWSRIVATCGTTTAT 504

Db 421 ALLTANNRNSWPASWGETSASSVPGTCAATSGTSSVTVTWSRIVATCGTTTAT 480

QY 505 PTGGSVTSKTTASKTSTTRS 530

Db 481 PTGGSVTSKTTASKTSTSS 506

RESULT 12

AAW55979 ID AAW55979 Standard; protein; 616 AA.

AC AAW55979;

XX DT 27-JUL-1998 (first entry)

XX DE Aspergillus awamori glucoamylase mutant S411A.

XX KW Aspergillus awamori; glucoamylase; Aspergillus sp; mutant; fungal; food; fructose; corn; sweetener; 1,4-alpha-D-glucan glucohydrolase;

KW genetic engineering.

XX OS Synthetic.

OS Aspergillus awamori.

XX PN WO9813639-A1.

XX PD 29-JAN-1998.

XX PR 24-JUL-1997; 97WO-US012983.

XX PR 24-JUL-1996; 96US-0022278P.

XX PR 02-AUG-1996; 96US-0023077P.

PA (IOWA) UNIV IOWA STATE RES FOUND INC.

XX PI Allen M., Fang T., Li Y., Liu H., Chen H., Coutinho P., Honzatko R.; Ford C.; DR WPI; 1998-120764/11.

XX PT Genetically engineered fungal glucoamylase - useful in, e.g. food industry for production of high fructose corn sweeteners.

XX PS Claim 10; Page: 97pp; English.

XX CC The present sequence represents a specifically claimed mutant glucoamylase from Aspergillus awamori (1,4-alpha-D-glucan glucohydrolase).

CC The present invention describes fungal glucoamylases (FG) comprising: a mutation pair Asn20Cys coupled with Ala27Cys forming a disulphide bond between the 2 members of the pair; and a 311-314loop or Ser411Ala mutation. FG can be used in industry for the production of high fructose corn sweeteners, while the glucose produced by glucoamylase can be crystallised or used in fermentation to produce organic products, e.g. citric acid, ascorbic acid, lysine, glutamic acid or ethanol for beverages and fuel. The mutations provide increased thermal stability, reduced isomaltose formation and increased pH optimum. N.B. The present sequence is not given in the specification but is derived from SEQ ID NO:1 as stated in the claim

XX SQ Sequence 616 AA;

Query Match 94.7%; Score 2625; DB 2; Length 616; Best Local Similarity 99.4%; Pred. No. 1.1e-202; Matches 503; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATLDWSLNEATVARTAILNNIGADGAWVGAGSDGTVWASPTNDNPDYFYTWTDSGLVL 84
Db 1 ATLDWSLNEATVARTAILNNIGADGAWVGAGSDGTVWASPTNDNPDYFYTWTDSGLVL 60

QY 85 KTLVLDLFRNGTSLSTIENITISAQAVQOGNSPNPSDLSSSAGLGRPKENDETAVTGSW 144
Db 61 KTLVLDLFRNGTSLSTIENITISAQAVQOGNSPNPSDLSSSAGLGRPKENDETAVTGSW 120

QY 145 GRPQRQGPALRATAMGPGQMLDNGTSTTDIPLVRUDLSTVAQYMQQTGIDLWEE 204
Db 121 GRPQRQGPALRATAMGPGQMLDNGTSTTDIPLVRUDLSTVAQYMQQTGIDLWEE 180

QY 205 VNGSSFTTIAVQHRALEVEGSAFATAVGSSCSWCDSOAPELCYQSFWTGSSPILANFDSS 264
Db 181 VNGSSFTTIAVQHRALEVEGSAFATAVGSSCSWCDSOAPELCYQSFWTGSSPILANFDSS 240

QY 265 RSGKDANTLGSISHTDPPEACADDSTPQESPRALANKHEVDFRSIYTFLNDGLSDSEA 324
Db 241 RSGKDANTLGSISHTDPPEACADDSTPQESPRALANKHEVDFRSIYTFLNDGLSDSEA 300

QY 325 WAVGRYPEDTYINGNPWFLCTAAQOLYDLYQMDKGSEEVTDVSLDFPKAYSDAAT 384
Db 301 WAVGRYPEDTYINGNPWFLCTAAQOLYDLYQMDKGSEEVTDVSLDFPKAYSDAAT 360

QY 385 GTYSSSSTSISIVDAVKTFADGFVSIETMASNSMSMSEQYDKSDGEQLSARDJTWYA 444
Db 361 GTYSSSSTSISIVDAVKTFADGFVSIETMASNSMSMSEQYDKSDGEQLSARDJTWYA 420

QY 445 ALTTANNRRNSVVPASWGETSASSVPGTCATAAIGTYSSVTVTSPSIVATGGTTAT 504
Db 421 ALTTANNRRNSVVPASWGETSASSVPGTCATAAIGTYSSVTVTSPSIVATGGTTAT 480

QY 505 PTGSGSVTSTSKTATASKTSTS 530
Db 481 PTGSGSVTSTSKTATASKTSTS 506

RESULT 13
AAB15180
ID AAB15180 standard; protein; 616 AA.
XX AAB15180;
AC
XX DT 11-DEC-2000 (first entry)
DE Aspergillus awamori mutant glucoamylase S411A substitution.
XX Glucoamylase; enzyme; carbohydrate; glucose;
KW 1,4-alpha-D-glucan glucohydrolase; mutein; mutation.
XX OS Aspergillus awamori.
OS Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 411 /note= "Wild-type Ser substituted by Ala"
PT XX BN WO200443504-A1.
XX PD 27-JUL-2000.
XX PP 10-JAN-2000; 2000WO-US000532.
XX PR 22-JAN-1999; 99US-00236063.
XX PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX PI Allen MJ., Fang T., Li Y., Liu H., Chen H., Coutinho P., Honzatko R.;
PT Ford C.; DR WPI; 2000-514725/46.

XX PT Fungal glucoamylase for selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose, has mutation pair Asn20Cys coupled with Ala27Cys forming disulfide bond between the two stabilizing members.

XX BS Claim 10; Page: 160pp; English.

XX CC Glucoamylase (1,4-alpha-D-glucan glucohydrolase; E.C. 3.2.1.3) is a carbohydrate. This enzyme cleaves D-glucose from the non-reducing ends of maltooligosaccharides, attacking alpha-(1,4)- and alpha-(1,6)-glucosidic bonds. The present invention relates to mutant glucoamylases, which have increased thermostability, increased pH optimum and reduced isomaltose formation. The mutant proteins are useful for the selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose. The present sequence is one such mutant enzyme. Note: The present sequence is not shown in the specification but is derived from the Aspergillus awamori wild-type glucoamylase sequence given in pages 152-153 of the sequence listing (SEQ ID 1)

XX SQ Sequence 616 AA;

Query Match 94.7%; Score 2625; DB 3; Length 616; Best Local Similarity 99.4%; Pred. No. 1.1e-202; Matches 503; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATLDWSLNEATVARTAILNNIGADGAWVGAGSDGTVWASPTNDNPDYFYTWTDSGLVL 84
Db 1 ATLDWSLNEATVARTAILNNIGADGAWVGAGSDGTVWASPTNDNPDYFYTWTDSGLVL 60

Not claimed 435

QY 85 KTLVUDLFRNGDTSLSLTENIYSAQIIVOGISNSPGDLSGAGLGERKENDEBAYGSW 144
 Db 61 KTLVUDLFRNGDTSLSLTENIYSAQIIVOGISNSPGDLSGAGLGERKENDEBAYGSW 120
 QY 145 GRPQRDGPAKATAMIGGQWLNDNGYSTATDIIWPLVRNDLSYVAQWNTQGYDWE 204
 Db 121 GRPQRDGPAKATAMIGGQWLNDNGYSTATDIIWPLVRNDLSYVAQWNTQGYDWE 180
 205 VNGSFFTAQVORHALVEGSAFATAVGSSCSWCSDQSAPELCYLQSFWTGCFILANFSS 264
 QY 181 VNGSFFTAQVORHALVEGSAFATAVGSSCSWCSDQSAPELCYLQSFWTGCFILANFSS 240
 265 RSGKDANTLIGSHTFPDRAACDSTFOCPSPRALANKEVUVDSRSTYLTNGLSDSEA 324
 241 RSGKDANTLIGSHTFPDPEACCDSTFOCPSPRALANKEVUVDSRSTYLTNGLSDSEA 300
 Qy 325 VAVGRYPDTTYGNPWFCLTAAEQLDYQDQKGSLETVDSLDPFKALYSDAAT 384
 Db 301 VAVGRYPDTTYGNPWFCLTAAEQLDYQDQKGSLETVDSLDPFKALYSDAAT 360
 QY 385 GTYSSSSSTYSSIVDAVKTFADGFVSVIETHAASNGSMSSEQDQYDSDGEQSLARDLTWSA 444
 Db 361 GTYSSSSSTYSSIVDAVKTFADGFVSVIETHAASNGSMSSEQDQYDSDGEQSLARDLTWSA 420
 QY 445 ALLTANNRNRNSVVPASWGETSASSVPGTCATSAIGTYSSVTWPSIVATGGTTAT 504
 Db 421 ALLTANNRNRNSVVPASWGETSASSVPGTCATSAIGTYSSVTWPSIVATGGTTAT 480
 Qy 505 PTGGSVTSKTKTATASKTSITRS 530
 Db 481 PTGGSVTSKTKTATASKTSITRS 506

RESULT 14

ID AAM55976 standard; protein; 616 AA.

XX AAM55976;
 XX DT 27-JUL-1998 (first entry)

DE Aspergillus awamori glucoamylase mutant N20C, A27C.

XX Aspergillus awamori; glucoamylase; Aspergillus sp; mutant; fungal; food; fructose; corn; sweetener; 1,4-alpha-D-glucan glucohydrolase; genetic engineering.

OS Synthetic.

OS Aspergillus awamori.

XX Key Location/Qualifiers
 FH Disulfide-bond 20..27
 XX PN WO803639-A1.
 XX PD 29-JAN-1998.
 XX PP 24-JUL-1997; 97WO-US012983.
 PR 24-JUL-1996; 96US-0022578P.
 PR 02-AUG-1996; 96US-0023077P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

PI Allen M, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R; Ford C; DR WPI; 1998-120764/11.

XX PT Genetically engineered fungal glucoamylase - useful in, e.g. food industry for production of high fructose corn sweeteners.

PS Claim 1; Page; 97pp; English.

QY 85 KTLVUDLFRNGDTSLSLTENIYSAQIIVOGISNSPGDLSGAGLGERKENDEBAYGSW 144
 CC The present sequence represents a specifically claimed mutant
 CC glucoamylase from Aspergillus awamori (1,4-alpha-D-glucan
 CC glucohydrolase). The present invention describes fungal Gluccamylases
 CC comprising: a mutation pair Asn20Cys coupled with Ala27Cys forming a
 CC disulphide bond between the 2 members of the pair; and a 311-314 loop or
 CC Ser41Ala mutation. EG can be used in industry for the production of high
 CC fructose Corn Sweeteners, while the Glucose produced by Glucoamylase can
 CC be crystallised or used in fermentation to produce organic products, e.g.
 CC citric acid, ascorbic acid, lysine, glutamic acid or ethanol for
 CC beverages and fuel. The mutations provide increased thermal stability,
 CC reduced isomaltose formation and increased pH optimum. N.B. The present
 CC sequence is not given in the specification but is derived form SEQ ID
 CC NO:1 as stated in the claim
 XX SQ Sequence 616 AA:

Query Match	Score	DB	Length
Best local similarity	99.2%	2	616
Matches	502	2	616
Conservative	1	2	616
Mismatches	3	2	616
Indels	0	2	616
Gaps	0	2	616

Db 1 ATLSWSNEATARTALCNIGADGWGWSGDSQASVAPSPDNPDYFTWDRGIVL 60
 QY 85 KTLVUDLFRNGDTSLSLTENIYSAQIIVOGISNSPGDLSGAGLGERKENDEBAYGSW 144
 Db 61 KTLVUDLFRNGDTSLSLTENIYSAQIIVOGISNSPGDLSGAGLGERKENDEBAYGSW 120
 QY 145 GRPQRDGPAKATAMIGGQWLNDNGYSTATDIIWPLVRNDLSYVAQWNTQGYDWE 204
 Db 121 GRPQRDGPAKATAMIGGQWLNDNGYSTATDIIWPLVRNDLSYVAQWNTQGYDWE 180
 QY 205 VNGSFFTAQVORHALVEGSAFATAVGSSCSWCSDQSAPELCYLQSFWTGCFILANFSS 264
 Db 181 VNGSFFTAQVORHALVEGSAFATAVGSSCSWCSDQSAPELCYLQSFWTGCFILANFSS 240
 QY 265 RSGKDANTLIGSHTFPDRAACDSTFOCPSPRALANKEVUVDSRSTYLTNGLSDSEA 324
 Db 241 RSGKDANTLIGSHTFPDPEACCDSTFOCPSPRALANKEVUVDSRSTYLTNGLSDSEA 300
 QY 325 VAVGRYPDTTYGNPWFCLTAAEQLDYQDQKGSLETVDSLDPFKALYSDAAT 384
 Db 301 VAVGRYPDTTYGNPWFCLTAAEQLDYQDQKGSLETVDSLDPFKALYSDAAT 360
 QY 385 GTYSSSSSTYSSIVDAVKTFADGFVSVIETHAASNGSMSSEQDQYDSDGEQSLARDLTWSA 444
 Db 361 GTYSSSSSTYSSIVDAVKTFADGFVSVIETHAASNGSMSSEQDQYDSDGEQSLARDLTWSA 420
 QY 445 ALLTANNRNRNSVVPASWGETSASSVPGTCATSAIGTYSSVTWPSIVATGGTTAT 504
 Db 421 ALLTANNRNRNSVVPASWGETSASSVPGTCATSAIGTYSSVTWPSIVATGGTTAT 480
 QY 505 PTGGSVTSKTKTATASKTSITRS 530
 Db 481 PTGGSVTSKTKTATASKTSITRS 506

RESULT 15

ID AAB15178 standard; protein; 616 AA.

XX AAB15178;
 XX DT 11-DEC-2000 (first entry)

DE Aspergillus awamori mutant glucoamylase N20C/A27C substitution.

XX Glucoamylase; enzyme; carbohydrate; glucose;
 KW 1,4-alpha-D-glucan glucohydrolase; mutein; mutation.

OS Synthetic.

Poss Note

XX	Key	Db
XX	Location/Qualifiers	361 GTYSSSSSTSSIVDAWKTADGFVISVETHAASNSMSOEYDKSDGEOBSARDLTWSYA 420
FH		Qy 445 ALLTANNRNSVNPASWGETSASSVPGTCATSAITGYTSSTVTPSWPSTVATGRTTAT 504
FT		Db 421 ALLTANNRNSVNPASWGETSASSVPGTCATSAITGYTSSTVTPSWPSTVATGRTTAT 480
FT	/note= "Wild-type Asn substituted by Cys"	FT Misc-difference 27
XX		XX WO20043504-A1.
XX		XX 27-JUL-2000.
PR		XX 10-JAN-2000; 2000WO-US000532.
XX		XX 22-JAN-1999; 99US-00236063.
PA	(IOWA) UNIV IOWA STATE RBS FOUND INC.	XX
PI	Allen MJ, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R;	XX
PI	Ford C;	XX
PS	WPI; 2000-514725/46.	XX
PT	Fungal glucoamylase for selective production of glucose rather than alpha	XX
PT	-1,6 linked diaccharide isomaltose, has mutation pair Asn2xCys coupled	XX
PT	with Ala2xCys forming disulfide bond between the two stabilizing members.	XX
CC	Claim 1; Page; 160pp; English.	XX
CC	Glucosidase (1, 4-alpha-D-glucan glucohydrolase; E.C. 3.2.1.3) is a	CC
CC	carbohydrase. This enzyme cleaves D-glucose from the nonreducing ends of	CC
CC	maltooligosaccharides, attacking alpha-(1,4)- and alpha-(1,6)-glucosidic	CC
CC	bonds. The present invention relates to mutant glucosidases, which have	CC
CC	increased thermostability, increased pH optimum and reduced isomaltose	CC
CC	formation. The mutant proteins are useful for the selective production of	CC
CC	glucose rather than alpha-1,6 linked diaccharide isomaltose. The present	CC
CC	sequence is one such mutant enzyme. Note: The present sequence is not	CC
CC	shown in the specification but is derived from the Aspergillus awamori	CC
CC	wild-type glucosidase sequence given in pages 152-153 of the sequence	CC
SQ	listing (SEQ ID 1)	XX
SQ	Sequence 616 AA:	XX

Query Match 94.4%; Score 2615; DB 3; Length 616;

Best Local Similarity 99.2%; Pred. No. 7.3e-202; Matches 502; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ATLDLSLNEATVARTAILNIGADAWWSADSGITVVASPTNDYFWTRDSQLVL 84

Db 1 ATLDLSLNEATVARTAILNIGADAWWSADSGITVVASPTNDYFWTRDSQLVL 60

Qy 85 KTLVDFRNGTSLSLTIENTISQAIVQGSNPSGLISSAGLGPKEFNDETAYGSW 144

Db 61 KTLVDFRNGTSLSLTIENTISQAIVQGSNPSGLISSAGLGPKEFNDETAYGSW 120

Qy 145 GRPQRDGPAALDATAMIGFGQNLNDGTYSTADIVPLVRNDLSVVAQYMMQTGDLWEE 204

Db 121 GRPQRDGPAALDATAMIGFGQNLNDGTYSTADIVPLVRNDLSVVAQYMMQTGDLWEE 180

Qy 205 VNGSSFTTIAVQHRALEVGSIIFATAVGSSCWCDSQAPETICYLQSFWTSSFLANFDSS 264

Db 181 VNGSSFTTIAVQHRALEVGSIIFATAVGSSCWCDSQAPETICYLQSFWTSSFLANFDSS 240

Qy 265 RSGKDANTLGSIHTDPPEACDDSFQPCSPRALNHKEYWDPSRSIYIINDGJSEA 324

Db 241 RSGKDANTLGSIHTDPPEACDDSFQPCSPRALNHKEYWDPSRSIYIINDGJSEA 300

Qy 325 VAVGRYPDTTYNGNIPFLCTAAEQLDYIQLQWDKQGSIEVTDVSLDFPKALYDAAT 384

Db 301 VAVGRYPDTTYNGNIPFLCTAAEQLDYIQLQWDKQGSIEVTDVSLDFPKALYDAAT 360

Qy 385 GRYSSSSTYSIVDAVKTEADGFVSVETHASNGSMSBQYDKSGEOLSLARDLTWSYA 444

MIS PAGE LEFT BLANK

post dated Page 1
a/pvcam

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2004, 17:47:36 ; Search time 50 Seconds

(without alignments)
3015.110 Million cell updates/sec

Title: US-10-038-723-2

Perfect score: 2771

Sequence: 1 MSFRSLALSGLVCTGIANV.....SKTTATASKTSTTRSCNSL 534

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgm2_6/prodata/1/pubpaal/us07_pubcomb.pep:*

2: /cgm2_6/prodata/1/pubpaal/pct_new_pub.pep:*

3: /cgm2_6/prodata/1/pubpaal/us06_pubcomb.pep:*

4: /cgm2_6/prodata/1/pubpaal/us06_pubcomb.pep:*

5: /cgm2_6/prodata/1/pubpaal/us07_new_pub.pep:*

6: /cgm2_6/prodata/1/pubpaal/pctus_pubcomb.pep:*

7: /cgm2_6/prodata/1/pubpaal/us08_new_pub.pep:*

8: /cgm2_6/prodata/1/pubpaal/pct_new_pub.pep:*

9: /cgm2_6/prodata/1/pubpaal/us09_pubcomb.pep:*

10: /cgm2_6/prodata/1/pubpaal/us09_pubcomb.pep:*

11: /cgm2_6/prodata/1/pubpaal/us09_pubcpc_pubcomb.pep:*

12: /cgm2_6/prodata/1/pubpaal/us09_new_pub.pep:*

13: /cgm2_6/prodata/1/pubpaal/us10_pubcomb.pep:*

14: /cgm2_6/prodata/1/pubpaal/us10_pubcomb.pep:*

15: /cgm2_6/prodata/1/pubpaal/us10c_pubcomb.pep:*

16: /cgm2_6/prodata/1/pubpaal/us10c_pubcomb.pep:*

17: /cgm2_6/prodata/1/pubpaal/us60_new_pub.pep:*

18: /cgm2_6/prodata/1/pubpaal/us60_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

§

Result No. Score Query Match Length DB ID Description

1 2771 100.0 534 9 US-09-908-395-2 Sequence 2, Appli

2 2771 100.0 534 10 US-09-908-395-2 Sequence 9, Appli

3 2771 100.0 534 14 US-10-038-723-2 Sequence 2, Appli

4 2771 100.0 534 15 US-10-421-586-2 Sequence 2, Appli

5 2771 100.0 534 15 US-10-421-586-3 Sequence 3, Appli

6 2742 99.0 640 14 US-10-038-723-13 Sequence 13, Appli

7 2742 99.0 640 15 US-10-421-586-14 Sequence 14, Appli

8 2735 98.7 743 15 US-10-418-836-9 Sequence 9, Appli

9 2735 98.7 763 15 US-10-418-836-13 Sequence 13, Appli

10 2735 98.7 979 15 US-10-418-836-10 Sequence 10, Appli

11 2735 98.7 979 15 US-10-418-836-16 Sequence 16, Appli

12 2720.5 98.2 738 15 US-10-418-836-19 Sequence 19, Appli

13 2716 98.0 741 15 US-10-418-836-30 Sequence 30, Appli

14 2715.5 98.0 972 15 US-10-418-836-38 Sequence 38, Appli

15 2715 98.0 US-10-418-836-26 Sequence 26, Appli

RESULT 1
US-09-908-395-2

Sequence 2, Application US/09908395

Parent No. US20020164723A1

GENERAL INFORMATION:

APPLICANT: Liaw, Gin

APPLICANT: Pedersen, Sven

APPLICANT: Hendriksen, Sven

TITLE OF INVENTION: A Method of Producing Saccharide

TITLE OF INVENTION: Preparations

FILE REFERENCE: 5318-200-US

CURRENT APPLICATION NUMBER: US/09/908,395

CURRENT FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US/09/198,672

PRIOR FILING DATE: PRIOR FILING DATE: 1998-11-23

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO: 2 LENGTH: 534

TYPE: PRT

ORGANISM: Aspergillus Niger

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)..(24)

US-09-908-395-2

Query Match Similarity 100.0%; Score 2771; DB 9; Length 534;

Best Local Similarity 100.0%; Pred. No. 2.7e-237;

Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQ 1 MSFRSLALSGLVCTGIANVSKRATLDSLSNEATVARTAILNNIGADGAWSGADSGI 60

Db 1 MSFRSLALSGLVCTGIANVSKRATLDSLSNEATVARTAILNNIGADGAWSGADSGI 60

OQ 61 WVASSTDNDYFYWTRDGLVLUKTLVDFRNGDTSLUSTIENIYSAQIVQGSINPSG 120

Db 61 WVASSTDNDYFYWTRDGLVLUKTLVDFRNGDTSLUSTIENIYSAQIVQGSINPSG 120

Qy 121 DLSSGAGLGEPKENDETAATGSWGRPQDGPA RATAMIGFQWLNGYSTATDVW 180
 Db 121 DLSSGAGLGEPKENDETAATGSWGRPQDGPA RATAMIGFQWLNGYSTATDVW 180
 Qy 181 PLVRNDLSVAVQMNQGTDLWEVNGSSPFTIAVQRALVESSAFATAVGSSCWDSQ 240
 Db 181 PLVRNDLSVAVQMNQGTDLWEVNGSSPFTIAVQRALVESSAFATAVGSSCWDSQ 240
 Qy 241 APEILCYQSFWTGSPFLANPDSRSRGKDANTLGSIHTFDPEACDSTFOPCS P RALA 300
 Db 241 APEILCYQSFWTGSPFLANPDSRSRGKDANTLGSIHTFDPEACDSTFOPCS P RALA 300
 Qy 301 NHKEVWDSPRSITYLNDGLSDSEAVAVGRYPEDTIYNQNPWFCTLAQEQLDALYQWD 360
 Db 301 NHKEVWDSPRSITYLNDGLSDSEAVAVGRYPEDTIYNQNPWFCTLAQEQLDALYQWD 360
 Qy 361 KQSSLLEVTDVSLDFPKALYSDAATGTYSSSSTSYSSIVDAVKTPADGFVISIVTHAASNG 420
 Db 361 KQSSLLEVTDVSLDFPKALYSDAATGTYSSSSTSYSSIVDAVKTPADGFVISIVTHAASNG 420
 Qy 421 SMSRQYDKSDGEQSLARDLTWSYALLTANNRRNSVUPASWGETSASSVPGTCATSAIG 480
 Db 421 SMSRQYDKSDGEQSLARDLTWSYALLTANNRRNSVUPASWGETSASSVPGTCATSAIG 480
 Qy 481 TYSVTVTWSWPSIVATGGTTTAPTGGSVTSKTTASKTSTTRSGMSL 534
 Db 481 TYSVTVTWSWPSIVATGGTTTAPTGGSVTSKTTASKTSTTRSGMSL 534
 RESULT 2
 US-09-821-616-9
 ; Sequence 9, Application US/09821616
 ; Publication No. US20030027290A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjarne R.
 ; APPLICANT: Nielsen, Ruby
 ; APPLICANT: Lehmbbeck, Jan
 ; TITLE OF INVENTION: Thermostable Glucoamylase
 ; FILE REFERENCE: 52/9.200-US
 ; CURRENT APPLICATION NUMBER: US/09/821,616
 ; CURRENT FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/199,290
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-25
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE: SIGNAL
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
 ; US-09-821-616-9

RESULT 3
 US-10-038-723-2
 ; Sequence 2, Application US/10038723
 ; Publication No. US20030032163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjarne Roenfeldt
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Pedersen, Henrik
 ; APPLICANT: Vind, Jesper
 ; APPLICANT: Hendriksen, Hanne Vang
 ; APPLICANT: Frandsen, Torben Peter
 ; TITLE OF INVENTION: Glucoamylase Variants
 ; FILE REFERENCE: 5636.200-US
 ; CURRENT APPLICATION NUMBER: US/10/038,723
 ; CURRENT FILING DATE: 2002-01-02
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/351,814
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00937
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 01667
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,528
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/115,545
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-12
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
 ; US-10-038-723-2

Query Match 100.0%; Score 2771; DB 10; Length 534;
 Best Local Similarity 100.0%; Pred. No. 2.7e-237; Indels 0; Gaps 0;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFRSLLAISGLGVCTGLANVSKRATDSLWLNATVARTAIIANNIGADGAWVGADSGI 60
 Db 1 MSFRSLLAISGLGVCTGLANVSKRATDSLWLNATVARTAIIANNIGADGAWVGADSGI 60

QY 1 MSFRSLALSGLIVCTGLANVSKRATLDSWSNEATVARTAILNNIGADGAWVGADSGI 60
 1 MSFRSLALSGLIVCTGLANVSKRATLDSWSNEATVARTAILNNIGADGAWVGADSGI 60
 QY 61 VVASPSTDNPYFTWTRDSVLKTLVDRNGTSLISTENIQAIVQGSNSPG 120
 61 VVASPSTDNPYFTWTRDSVLKTLVDRNGTSLISTENIQAIVQGSNSPG 120
 Db 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 Db 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 QY 181 PLVRNDLSYVQYQWNGTYDWEENNGSSFTIAYORHALVEGSAFTAVGSSCSNDSQ 240
 Db 181 PLVRNDLSYVQYQWNGTYDWEENNGSSFTIAYORHALVEGSAFTAVGSSCSNDSQ 240
 QY 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 Db 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 QY 241 APEILCYLQSFTWTGSFLANFDSSRGKDANTLGSIHTEPDPEACCDSTFOPCSPRALA 300
 241 APEILCYLQSFTWTGSFLANFDSSRGKDANTLGSIHTEPDPEACCDSTFOPCSPRALA 300
 Db 181 PLVRNDLSYVQYQWNGTYDWEENNGSSFTIAYORHALVEGSAFTAVGSSCSNDSQ 240
 181 PLVRNDLSYVQYQWNGTYDWEENNGSSFTIAYORHALVEGSAFTAVGSSCSNDSQ 240
 QY 301 NHKEVUDSFRSIYTINDGLSBSAVAVGRYPEDTYINGNPWFLCTLAABEQLDYALQWD 360
 301 NHKEVUDSFRSIYTINDGLSBSAVAVGRYPEDTYINGNPWFLCTLAABEQLDYALQWD 360
 Db 361 KQGSLEVTDVSLDFPKALYSDATGYSSSSTYSSIVDAVKTFADGFSVIVETHAASNG 420
 361 KQGSLEVTDVSLDFPKALYSDATGYSSSSTYSSIVDAVKTFADGFSVIVETHAASNG 420
 QY 421 SMSEQDTSKDCBQSLRSARDLWSYALLTANNRNSVPASWGETSASSVGTCAATSIG 480
 421 SMSEQDTSKDCBQSLRSARDLWSYALLTANNRNSVPASWGETSASSVGTCAATSIG 480
 Db 421 SMSEQDTSKDCBQSLRSARDLWSYALLTANNRNSVPASWGETSASSVGTCAATSIG 480
 421 SMSEQDTSKDCBQSLRSARDLWSYALLTANNRNSVPASWGETSASSVGTCAATSIG 480
 QY 481 TYSSVVTWSMSIVATGGTTATPGSGSVTSTSCTKTTASKSTTRGMSL 534
 481 TYSSVVTWSMSIVATGGTTATPGSGSVTSTSCTKTTASKSTTRGMSL 534
 Db 481 TYSSVVTWSMSIVATGGTTATPGSGSVTSTSCTKTTASKSTTRGMSL 534
 481 TYSSVVTWSMSIVATGGTTATPGSGSVTSTSCTKTTASKSTTRGMSL 534
 QY 421 SMSEQDTSKDCBQSLRSARDLWSYALLTANNRNSVPASWGETSASSVGTCAATSIG 480
 421 SMSEQDTSKDCBQSLRSARDLWSYALLTANNRNSVPASWGETSASSVGTCAATSIG 480
 Db 480 480
 ; Sequence 2, Application US/10421586
 ; Publication No. US20040002142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjarne Ronfeldt
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Pedersen, Henrik
 ; APPLICANT: Vind, Jesper
 ; APPLICANT: Hendriksen, Hanne Vang
 ; APPLICANT: Frandsen, Torben Peter
 ; APPLICANT: Bjarne Ronfeldt
 ; APPLICANT: Nielsen, Bjarne Ronfeldt
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Pedersen, Henrik
 ; APPLICANT: Hendriksen, Hanne Vang
 ; APPLICANT: Frandsen, Torben Peter
 ; TITLE OF INVENTION: Glucoamylase Variants
 ; FILE PREFERENCE: 5967.210-US
 ; CURRENT APPLICATION NUMBER: US/10/421, 586
 ; CURRENT FILING DATE: 2003-04-23
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 3
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE: Signal
 ; NAME/KEY: Signal
 ; LOCATION: (1)..(24)
 ;
 US-10-421-586-3
 ; Query Match 100.0%; Score 2771; DB 15; Length 534;
 ; Best Local Similarity 100.0%; Pred. No. 2.7e-237; Mismatches 534; Conservative 0; Indels 0; Gaps 0;
 ; Matches 534; Conserve 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFRSLALSGLIVCTGLANVSKRATLDSWSNEATVARTAILNNIGADGAWVGADSGI 60
 1 MSFRSLALSGLIVCTGLANVSKRATLDSWSNEATVARTAILNNIGADGAWVGADSGI 60
 Db 61 VVASPSTDNPYFTWTRDSVLKTLVDRNGTSLISTENIQAIVQGSNSPG 120
 61 VVASPSTDNPYFTWTRDSVLKTLVDRNGTSLISTENIQAIVQGSNSPG 120
 Db 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 Db 121 DLSSGAGLGEKFNFVDETAYGWSGRPQRDPALRATAMIGFGQWLLDNGYSTADIVW 180
 QY 181 PLVRNDLSYVQYQWNGTYDWEENNGSSFTIAYORHALVEGSAFTAVGSSCSNDSQ 240
 181 PLVRNDLSYVQYQWNGTYDWEENNGSSFTIAYORHALVEGSAFTAVGSSCSNDSQ 240

Db 301 NHKEVUDSFRSYTLYNDGLSDEAVAVGRYPEDTYNGNPWFCLTAAEQLYDLYQWD 360
 Qy 361 KQGSLEVDVSDFFKALYSDAATGTYSSSTYSSIVDAVKTFAQFVSVETHASNG 420
 Db 361 KQGSLEVDVSDFFKALYSDAATGTYSSSTYSSIVDAVKTFAQFVSVETHASNG 420
 Qy 421 SMSEQDQKSDGQLSARDLTSYAAUJTANRNSVTPASNGETSASSVPGTCATSAIG 480
 Db 421 SMSEQDQKSDGQLSARDLTSYAAUJTANRNSVTPASNGETSASSVPGTCATSAIG 480
 Qy 481 TYSSVTWSWPSIVATGCTTATPTGSGSVTSTSKTATASKSTTR 530
 Db 481 TYSSVTWSWPSIVATGCTTATPTGSGSVTSTSKTATASKSTTR 530
 ;
RESULT 8
 US-10-418-836-9
 ; Sequence 9, Application US/10418836
 ; Publication No. US20040018573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Power, Scott D.
 ; APPLICANT: Wang, Huaining
 ; APPLICANT: Ward, Michael
 ; TITLE OF INVENTION: Production of Functional Antibodies in
 ; Filamentous Fungi
 ; FILE REFERENCE: GC741-2
 ; CURRENT APPLICATION NUMBER: US/10/418,836
 ; CURRENT FILING DATE: 2003-04-17
 ; PRIOR APPLICATION NUMBER: US 60/373,889
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/411,540
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/452,134
 ; PRIOR FILING DATE: 2003-03-04
 ; PRIOR APPLICATION NUMBER: US 60/411,537
 ; PRIOR FILING DATE: 2002-09-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 9
 ; LENGTH: 743
 ;
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein
 ; US-10-418-836-9
 ;
 Query Match 98.7%; Score 2735; DB 15; Length 743;
 Best Local Similarity 99.6%; Pred. No. 7.2e-234;
 Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MSFRSLALSLCIVGTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
 Db 1 MSFRSLALSLCIVGTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
 Qy 61 VVASPSTDNPYFYTWDRSGLVLKVLVDRFLRGNTSLISTENYISAQAVQGSNPSG 120
 Db 61 VVASPSTDNPYFYTWDRSGLVLKVLVDRFLRGNTSLISTENYISAQAVQGSNPSG 120
 Qy 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMICFGQWLNDNGYSTATDIW 180
 Db 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMICFGQWLNDNGYSTATDIW 180
 Qy 181 PLVRNDLSYVQYWNQTYDWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240
 Db 181 PLVRNDLSYVQYWNQTYDWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240
 Qy 241 APEILCYLQSFWTGSPFLANDSSRSCKDANTLGSINTPEACDDSTFOPCSPRALA 300
 Db 241 APEILCYLQSFWTGSPFLANDSSRSCKDANTLGSINTPEACDDSTFOPCSPRALA 300
 Qy 301 NHKEVUDSFRSYTLYNDGLSDEAVAVGRYPEDTYNGNPWFCLTAAEQLYDLYQWD 360
 Db 301 NHKEVUDSFRSYTLYNDGLSDEAVAVGRYPEDTYNGNPWFCLTAAEQLYDLYQWD 360

Db 361 KQGSLEVDVSDFFKALYSDAATGTYSSSTYSSIVDAVKTFAQFVSVETHASNG 420
 Qy 361 KQGSLEVDVSDFFKALYSDAATGTYSSSTYSSIVDAVKTFAQFVSVETHASNG 420
 Db 421 SMSEQDQKSDGQLSARDLTSYAAUJTANRNSVTPASNGETSASSVPGTCATSAIG 480
 Qy 421 SMSEQDQKSDGQLSARDLTSYAAUJTANRNSVTPASNGETSASSVPGTCATSAIG 480
 Db 481 TYSSVTWSWPSIVATGCTTATPTGSGSVTSTSKTATASKSTTR 529
 Qy 481 TYSSVTWSWPSIVATGCTTATPTGSGSVTSTSKTATASKSTTR 529
 ;
RESULT 9
 US-10-418-836-13
 ; Sequence 13, Application US/10418836
 ; Publication No. US20040018573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Power, Scott D.
 ; APPLICANT: Wang, Huaining
 ; APPLICANT: Ward, Michael
 ; TITLE OF INVENTION: Production of Functional Antibodies in
 ; Filamentous Fungi
 ; FILE REFERENCE: GC741-2
 ; CURRENT APPLICATION NUMBER: US/10/418,836
 ; CURRENT FILING DATE: 2003-04-17
 ; PRIOR APPLICATION NUMBER: US 60/373,889
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/411,540
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/452,134
 ; PRIOR FILING DATE: 2003-03-04
 ; PRIOR APPLICATION NUMBER: US 60/411,537
 ; PRIOR FILING DATE: 2002-09-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 13
 ; LENGTH: 763
 ;
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein
 ; US-10-418-836-13
 ;
 Query Match 98.7%; Score 2735; DB 15; Length 763;
 Best Local Similarity 99.6%; Pred. No. 7.5e-234;
 Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MSFRSLALSLCIVGTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
 Db 1 MSFRSLALSLCIVGTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
 Qy 61 VVASPSTDNPYFYTWDRSGLVLKVLVDRFLRGNTSLISTENYISAQAVQGSNPSG 120
 Db 61 VVASPSTDNPYFYTWDRSGLVLKVLVDRFLRGNTSLISTENYISAQAVQGSNPSG 120
 Qy 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMICFGQWLNDNGYSTATDIW 180
 Db 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMICFGQWLNDNGYSTATDIW 180
 Qy 181 PLVRNDLSYVQYWNQTYDWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240
 Db 181 PLVRNDLSYVQYWNQTYDWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240
 Qy 241 APEILCYLQSFWTGSPFLANDSSRSCKDANTLGSINTPEACDDSTFOPCSPRALA 300
 Db 241 APEILCYLQSFWTGSPFLANDSSRSCKDANTLGSINTPEACDDSTFOPCSPRALA 300
 Qy 301 NHKEVUDSFRSYTLYNDGLSDEAVAVGRYPEDTYNGNPWFCLTAAEQLYDLYQWD 360
 Db 301 NHKEVUDSFRSYTLYNDGLSDEAVAVGRYPEDTYNGNPWFCLTAAEQLYDLYQWD 360

RESULT 10
US-10-418-836-10
; Sequence 10, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; FILE REFERENCE: GT41-2
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373, 889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411, 540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452, 134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411, 537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
; US-10-418-836-10

Query Match 99.7%; Score 2735; DB 15; Length 979;
Best Local Similarity 99.6%; Pred. No. 1.1e-233; Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSFRSLLAISGLVCTGLANVISKRATLDSLWLSNEARTVARTAILNNIGDAGAWNSGADGGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSLWLSNEARTVARTAILNNIGDAGAWNSGADGGI 60
QY 61 VVASPSTDNPDYFTWTRDSGLVLTKLDFLRNGDTSLISTENYISQAIVOGISNSG 120
Db 61 VVASPSTDNPDYFTWTRDSGLVLTKLDFLRNGDTSLISTENYISQAIVOGISNSG 120
QY 61 VVASPSTDNPDYFTWTRDSGLVLTKLDFLRNGDTSLISTENYISQAIVOGISNSG 120
Db 61 VVASPSTDNPDYFTWTRDSGLVLTKLDFLRNGDTSLISTENYISQAIVOGISNSG 120
QY 121 DLSSGAGIGEPKFNDETAATGSGWRPORDGPALRATAMIGFCOWLINGYSTATDIW 180
Db 121 DLSSGAGIGEPKFNDETAATGSGWRPORDGPALRATAMIGFCOWLINGYSTATDIW 180
QY 181 PLVRNDLSVVAQYMNQTDLWEENGSSFTAVQRHALVEGAPATAVGSSCSWCDSQ 240
Db 181 PLVRNDLSVVAQYMNQTDLWEENGSSFTAVQRHALVEGAPATAVGSSCSWCDSQ 240
QY 241 APEIICYQSFWSFGSFLANFDSSRSRGKDANTLGSIRMPDEACDSTFQCPSPRALA 300
Db 241 APEIICYQSFWSFGSFLANFDSSRSRGKDANTLGSIRMPDEACDSTFQCPSPRALA 300
QY 301 NHKEVUDSRSPRSIYTLDGSDSEAVAVGRYPEDTYINGNPWFCLTAAEQQLDALQWD 360
Db 301 NHKEVUDSRSPRSIYTLDGSDSEAVAVGRYPEDTYINGNPWFCLTAAEQQLDALQWD 360
QY 361 KQGSLEVTDVSLDFKALYSRPTGTSSSSTSYSSIVDAVKFADGEVSIVETHAASNG 420

RESULT 11
US-10-418-836-16
; Sequence 16, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; FILE REFERENCE: GT41-2
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373, 889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411, 540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452, 134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411, 537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
; US-10-418-836-16

Query Match 98.7%; Score 2735; DB 15; Length 979;
Best Local Similarity 99.6%; Pred. No. 1.1e-233; Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSFRSLLAISGLVCTGLANVISKRATLDSLWLSNEARTVARTAILNNIGDAGAWNSGADGGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSLWLSNEARTVARTAILNNIGDAGAWNSGADGGI 60
QY 61 VVASPSTDNPDYFTWTRDSGLVLTKLDFLRNGDTSLISTENYISQAIVOGISNSG 120
Db 61 VVASPSTDNPDYFTWTRDSGLVLTKLDFLRNGDTSLISTENYISQAIVOGISNSG 120
QY 121 DLSSGAGIGEPKFNDETAATGSGWRPORDGPALRATAMIGFCOWLINGYSTATDIW 180
Db 121 DLSSGAGIGEPKFNDETAATGSGWRPORDGPALRATAMIGFCOWLINGYSTATDIW 180
QY 181 PLVRNDLSVVAQYMNQTDLWEENGSSFTAVQRHALVEGAPATAVGSSCSWCDSQ 240
Db 181 PLVRNDLSVVAQYMNQTDLWEENGSSFTAVQRHALVEGAPATAVGSSCSWCDSQ 240
QY 241 APEIICYQSFWSFGSFLANFDSSRSRGKDANTLGSIRMPDEACDSTFQCPSPRALA 300
Db 241 APEIICYQSFWSFGSFLANFDSSRSRGKDANTLGSIRMPDEACDSTFQCPSPRALA 300
QY 301 NHKEVUDSRSPRSIYTLDGSDSEAVAVGRYPEDTYINGNPWFCLTAAEQQLDALQWD 360
Db 301 NHKEVUDSRSPRSIYTLDGSDSEAVAVGRYPEDTYINGNPWFCLTAAEQQLDALQWD 360
QY 361 KQGSLEVTDVSLDFKALYSRPTGTSSSSTSYSSIVDAVKFADGEVSIVETHAASNG 420

RESULT 12
US-10-418-836-19
; Sequence 19, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; FILE REFERENCE: GC741-2
; CURRENT APPLICATION NUMBER: US/10/418, 836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373, 889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411, 540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452, 134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411, 537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
; US-10-418-836-19

Query Match 98.2%; Score 2720.5; DB 15; Length 738;
Best Local Similarity 98.5%; Pred. No. 4.e-332; Matches 527; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 MSFRSLLALSLCIVCTGLANVSKRATLDSWISNEATVARTAILNNIGADGAWVSGADSGI 60
Db 1 MSFRSLLALSLCIVCTGLANVSKRATLDSWISNEATVARTAILNNIGADGAWVSGADSGI 60
Qy 61 VVASPSTDNPYFYTWRDGLVLUKTLVDRFLRGNTDSLSTIENYISAQAVQGTSNPG 120
Db 61 VVASPSTDNPYFYTWRDGLVLUKTLVDRFLRGNTDSLSTIENYISAQAVQGTSNPG 120
Qy 181 PLVRNDLSYYAQWNGTGYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Db 121 DLSSGAGLGKEPKENDETAVGSKQRDGPALARATAMIGFGQWLDNGYSTATIDW 180
Db 121 DLSSGAGLGKEPKENDETAVGSKQRDGPALARATAMIGFGQWLDNGYSTATIDW 180
Qy 181 PLVRNDLSYYAQWNGTGYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Db 181 PLVRNDLSYYAQWNGTGYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Qy 241 APEIICYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTFPEAACDDSTFQPCSPRALA 300
Db 241 APEIICYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTFPEAACDDSTFQPCSPRALA 300
Qy 301 NHKEVVDSDFSIYTUNDGLSDSEAVAVGRYPEDTYINGPNPFLCTLAABOLVLYQWD 360
Db 301 NHKEVVDSDFSIYTUNDGLSDSEAVAVGRYPEDTYINGPNPFLCTLAABOLVLYQWD 360
Qy 361 KQGSLEVTDSLDFKALSDAATGTYSSSSTYSSIVDAVKTPADGFVSVETHAASNG 420
Db 361 KQGSLEVTDSLDFKALSDAATGTYSSSSTYSSIVDAVKTPADGFVSVETHAASNG 420

RESULT 13
US-10-418-836-30
; Sequence 30, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; FILE REFERENCE: GC741-2
; CURRENT APPLICATION NUMBER: US/10/418, 836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373, 889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411, 540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452, 134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411, 537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
; US-10-418-836-30

Query Match 98.0%; Score 2716; DB 15; Length 741;
Best Local Similarity 98.0%; Pred. No. 3.e-232; Matches 527; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

Qy 1 MSFRSLLALSLCIVCTGLANVSKRATLDSWISNEATVARTAILNNIGADGAWVSGADSGI 60
Db 1 MSFRSLLALSLCIVCTGLANVSKRATLDSWISNEATVARTAILNNIGADGAWVSGADSGI 60
Qy 61 VVASPSTDNPYFYTWRDGLVLUKTLVDRFLRGNTDSLSTIENYISAQAVQGTSNPG 120
Db 61 VVASPSTDNPYFYTWRDGLVLUKTLVDRFLRGNTDSLSTIENYISAQAVQGTSNPG 120
Qy 121 DLSSGAGLGKEPKENDETAVGSKQRDGPALARATAMIGFGQWLDNGYSTATIDW 180
Db 121 DLSSGAGLGKEPKENDETAVGSKQRDGPALARATAMIGFGQWLDNGYSTATIDW 180
Qy 181 PLVRNDLSYYAQWNGTGYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Db 181 PLVRNDLSYYAQWNGTGYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Qy 241 APEIICYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTFPEAACDDSTFQPCSPRALA 300
Db 241 APEIICYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTFPEAACDDSTFQPCSPRALA 300
Qy 301 NHKEVVDSDFSIYTUNDGLSDSEAVAVGRYPEDTYINGPNPFLCTLAABOLVLYQWD 360
Db 301 NHKEVVDSDFSIYTUNDGLSDSEAVAVGRYPEDTYINGPNPFLCTLAABOLVLYQWD 360
Qy 361 KQGSLEVTDSLDFKALSDAATGTYSSSSTYSSIVDAVKTPADGFVSVETHAASNG 420
Db 361 KQGSLEVTDSLDFKALSDAATGTYSSSSTYSSIVDAVKTPADGFVSVETHAASNG 420

RESULT 14
US-10-18-836-38
; Sequence 38, Application US/10418836

; Publication No. US2004018573A1

; GENERAL INFORMATION:

; APPLICANT: Power, Scott D.

; APPLICANT: Wang, Ruaming

; APPLICANT: Ward, Michael

; TITLE OF INVENTION: Production of Functional Antibodies in Filamentous Fungi

; FILE REFERENCE: GCT41-2

; CURRENT APPLICATION NUMBER: US/10/418,836

; CURRENT FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: US 60/373,889

; PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US 60/411,540

; PRIOR FILING DATE: 2002-09-18

; PRIOR APPLICATION NUMBER: US 60/452,134

; PRIOR FILING DATE: 2003-03-04

; PRIOR APPLICATION NUMBER: US 60/411,537

; PRIOR FILING DATE: 2002-09-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 38

; LENGTH: 972

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: fusion protein

US-10-418-836-38

Query Match 98.0%; Score 2715; DB 15; Length 972;

Best Local Similarity 95.5%; Pred. No. 5.8e-232; Mismatches 4; Indels 21; Gaps 2; Matches 530; Conservative

Qy 1 MSFRSLLAISGLVCTGLANVISKRATIDLSWSLNEATVARTAILNNIGADGAWNSGADSGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATIDLSWSLNEATVARTAILNNIGADGAWNSGADSGI 60

Qy 61 VVASPSTNDPYFTWTRDSGLVLTLYDLFRNGDTSLSLSTENYISQAIVOGISNSG 120
Db 61 VVASPSTNDPYFTWTRDSGLVLTLYDLFRNGDTSLSLSTENYISQAIVOGISNSG 120

Qy 121 DLSSGAGLGEPKENDETAATGSGWRPQDGPAKRTAMIGFCQWLQNGYSTADIW 180
Db 121 DLSSGAGLGEPKENDETAATGSGWRPQDGPAKRTAMIGFCQWLQNGYSTADIW 180

Qy 181 PLVRNDLSYVAQMNQTYDLMWEVNGSPPFTIAVORHALVEGSAFATVGSSCWCSQ 240
Db 181 PLVRNDLSYVAQMNQTYDLMWEVNGSPPFTIAVORHALVEGSAFATVGSSCWCSQ 240

Qy 241 APELICYQSFWTSFILANDSFDRSRGKANTLGSIHFPFLACDSTFQPCSPRALA 300
Db 241 APELICYQSFWTSFILANDSFDRSRGKANTLGSIHFPFLACDSTFQPCSPRALA 300

Qy 301 NHKEVWDSRSTIYTINDGLSDSEAVAVGRGPEDTYNGNPFWFLCTLAABOQLDALYQWD 360
Db 301 NHKEVWDSRSTIYTINDGLSDSEAVAVGRGPEDTYNGNPFWFLCTLAABOQLDALYQWD 360

Qy 361 KQGSLLEVTDVSLDPFKALYSDAATCTYSSSSSTSIYDAVKITADGFVISVETHAASNG 420
Db 361 KQGSLLEVTDVSLDPFKALYSDAATCTYSSSSSTSIYDAVKITADGFVISVETHAASNG 420

Qy 421 MSSEQYDKSDGEQLSARDLTWSYALLTANNRRNSVPASWGETSASSVPGTCATSAIG 480
Db 421 MSSEQYDKSDGEQLSARDLTWSYALLTANNRRNSVPASWGETSASSVPGTCATSAIG 480

RESULT 15
US-10-418-836-26
; Sequence 26, Application US/10418836

; Publication No. US2004018573A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Ruaming

; APPLICANT: Ward, Michael

; TITLE OF INVENTION: Production of Functional Antibodies in Filamentous Fungi

; FILE REFERENCE: GCT41-2

; CURRENT APPLICATION NUMBER: US/10/418,836

; CURRENT FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: US 60/373,889

; PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US 60/411,540

; PRIOR FILING DATE: 2002-09-18

; PRIOR APPLICATION NUMBER: US 60/452,134

; PRIOR FILING DATE: 2003-03-04

; PRIOR APPLICATION NUMBER: US 60/411,537

; PRIOR FILING DATE: 2002-09-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 26

; LENGTH: 739

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: fusion protein

US-10-418-836-26

Query Match 98.0%; Score 2715; DB 15; Length 739;

Best Local Similarity 99.8%; Pred. No. 4.3e-232; Mismatches 0; Indels 0; Gaps 0; Matches 522; Conservative

Qy 1 MSFRSLLAISGLVCTGLANVISKRATIDLSWSLNEATVARTAILNNIGADGAWNSG 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATIDLSWSLNEATVARTAILNNIGADGAWNSG 60

Qy 61 VVASPSTNDPYFTWTRDSGLVLTLYDLFRNGDTSLSLSTENYISQAIVOGISNSG 120
Db 61 VVASPSTNDPYFTWTRDSGLVLTLYDLFRNGDTSLSLSTENYISQAIVOGISNSG 120

Qy 121 DLSSGAGLGEPKENDETAATGSGWRPQDGPAKRTAMIGFCQWLQNGYSTADIW 180
Db 121 DLSSGAGLGEPKENDETAATGSGWRPQDGPAKRTAMIGFCQWLQNGYSTADIW 180

Qy 181 PLVRNDLSYVAQMNQTYDLMWEVNGSPPFTIAVORHALVEGSAFATVGSSCWCSQ 240
Db 181 PLVRNDLSYVAQMNQTYDLMWEVNGSPPFTIAVORHALVEGSAFATVGSSCWCSQ 240

Qy 241 APELICYQSFWTSFILANDSFDRSRGKANTLGSIHFPFLACDSTFQPCSPRALA 300
Db 241 APELICYQSFWTSFILANDSFDRSRGKANTLGSIHFPFLACDSTFQPCSPRALA 300

Qy 301 NHKEVWDSRSTIYTINDGLSDSEAVAVGRGPEDTYNGNPFWFLCTLAABOQLDALYQWD 360
Db 301 NHKEVWDSRSTIYTINDGLSDSEAVAVGRGPEDTYNGNPFWFLCTLAABOQLDALYQWD 360

Qy 361 KQGSLLEVTDVSLDPFKALYSDAATCTYSSSSSTSIYDAVKITADGFVISVETHAASNG 420
Db 361 KQGSLLEVTDVSLDPFKALYSDAATCTYSSSSSTSIYDAVKITADGFVISVETHAASNG 420

Qy 421 MSSEQYDKSDGEQLSARDLTWSYALLTANNRRNSVPASWGETSASSVPGTCATSAIG 480
Db 421 MSSEQYDKSDGEQLSARDLTWSYALLTANNRRNSVPASWGETSASSVPGTCATSAIG 480

Fri Jun 18 17:42:19 2004

ub-10-038-723-2.rapb

Page 9

Db 361 KQGSLEVDVSLDPFKALYSRATGYISSSTYSSIVDAWKTFADGFVSVETHASNG 420
Qy 421 SMSEQYDKSDRQLSARDLTSYAAILTANRRNRYPASGETSASSVPCATSAIG 480
Db 421 SMSEQYDKSDRQLSARDLTSYAAILTANRRNRYPASGETSASSVPCATSAIG 480
Qy 481 TYSSVTVTSWISIVATGGTTATPGSGTSTSCKTATASK 523
Db 481 TYSSVTVTSWISIVATGGTTATPGSGTSTSCKTATASQ 523

Search completed: June 17, 2004, 17:53:29
Job time : 51 secB

Lynn
PAGE LEFT BLANK

Db 301 NHKEVUDSFRSIYIYLNGLSDSEAVAVGKYPEPTYINGNPWFCLTLAAEQLDALYQMD 360
 Qy 361 KQGSLEVTVSLDFKKALYSDAATGTYSSSTSYISIVDAVKTFADGFSIVETHAASNG 420
 Db 361 KQGSLEVTVSLDFKKALYSDAATGTYSSSTSYISIVDAVKTFADGFSIVETHAASNG 420
 Qy 421 SMSBQYDSDGEOLSDARLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAG 480
 Db 421 SMSBQYDSDGEOLSDARLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAG 480
 Qy 481 TYSVTVTWSWPSIVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
 Db 481 TYSVTVTWSWPSIVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
RESULT 2
 US-09-199-290-9
 ; Sequence 9, Application US/09199290
 ; Patent No. 6255084
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjørne R.
 ; APPLICANT: Nielsen, Ruby
 ; APPLICANT: Lehmbæk, Jan
 ; TITLE OF INVENTION: Thermostable Glucoamylase
 ; FILE REFERENCE: 5279 200-US
 ; CURRENT APPLICATION NUMBER: US/09/199, 290
 ; CURRENT FILING DATE: 1998-11-24
 ; EARLIER APPLICATION NUMBER: 1557/97
 ; EARLIER FILING DATE: 1997-12-30
 ; EARLIER APPLICATION NUMBER: 0225/98
 ; EARLIER FILING DATE: 1998-07-10
 ; EARLIER APPLICATION NUMBER: 60/070, 746
 ; EARLIER FILING DATE: 1998-01-08
 ; EARLIER APPLICATION NUMBER: 60/094, 344
 ; EARLIER FILING DATE: 1998-07-28
 ; EARLIER APPLICATION NUMBER: 08/979, 673
 ; EARLIER FILING DATE: 1997-11-26
 ; EARLIER APPLICATION NUMBER: 09/017, 657
 ; EARLIER FILING DATE: 1998-06-30
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
US-09-199-290-9
 Query Match 100.0%; Score 2771; DB 3; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1.1e-231;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFRSLALSLGLVCTGLANVSKRATLDSMSLNBEATVARTAILNIGDAGAWGAGSGI 60
 Db 1 MSFRSLALSLGLVCTGLANVSKRATLDSMSLNBEATVARTAILNIGDAGAWGAGSGI 60
 Qy 61 VVASPSTDNDPYFYTWTDSLGLVLUKTLYDLFRNGDTSLISTIENYISQAIVQISNSG 120
 Db 61 VVASPSTDNDPYFYTWTDSLGLVLUKTLYDLFRNGDTSLISTIENYISQAIVQISNSG 120
 Qy 121 DLSGGAGLGPKFENDETAYTGSWGRPQRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Db 121 DLSGGAGLGPKFENDETAYTGSWGRPQRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Qy 241 APEIICYLOSFWMGSFILENFDSSRGKDANTLGSIHPDEAACDDSTFQCPSPRALA 300
 Db 241 APEIICYLOSFWMGSFILENFDSSRGKDANTLGSIHPDEAACDDSTFQCPSPRALA 300
 Qy 301 NHKEVUDSFRSIYIYLNGLSDSEAVAVGKYPEPTYINGNPWFCLTLAAEQLDALYQMD 360
 Db 301 NHKEVUDSFRSIYIYLNGLSDSEAVAVGKYPEPTYINGNPWFCLTLAAEQLDALYQMD 360
 Qy 361 KQGSLEVTVSLDFKKALYSDAATGTYSSSTSYISIVDAVKTFADGFSIVETHAASNG 420
 Db 361 KQGSLEVTVSLDFKKALYSDAATGTYSSSTSYISIVDAVKTFADGFSIVETHAASNG 420
 Qy 421 SMSBQYDSDGEOLSDARLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAG 480
 Db 421 SMSBQYDSDGEOLSDARLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAG 480
 Qy 481 TYSVTVTWSWPSIVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
 Db 481 TYSVTVTWSWPSIVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
RESULT 3
 US-09-632-392-2
 ; Sequence 2, Application US/09632392
 ; Patent No. 6303346
 ; GENERAL INFORMATION:
 ; APPLICANT: Liaw, Gin
 ; APPLICANT: Pedersen, Sven
 ; APPLICANT: Hendriksen, Sven
 ; TITLE OF INVENTION: A Method of Producing Saccharide
 ; TITLE OF INVENTION: Preparations
 ; FILE REFERENCE: 5318 200-US
 ; CURRENT APPLICATION NUMBER: US/09/632, 392
 ; CURRENT FILING DATE: 2000-01-04
 ; PRIOR APPLICATION NUMBER: 09/198, 672
 ; PRIOR FILING DATE: 1998-11-23
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus Niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
US-09-632-392-2
 Query Match 100.0%; Score 2771; DB 4; length 534;
 Best Local Similarity 100.0%; Pred. No. 1.1e-231;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFRSLALSLGLVCTGLANVSKRATLDSMSLNBEATVARTAILNIGDAGAWGAGSGI 60
 Db 1 MSFRSLALSLGLVCTGLANVSKRATLDSMSLNBEATVARTAILNIGDAGAWGAGSGI 60
 Qy 61 VVASPSTDNDPYFYTWTDSLGLVLUKTLYDLFRNGDTSLISTIENYISQAIVQISNSG 120
 Db 61 VVASPSTDNDPYFYTWTDSLGLVLUKTLYDLFRNGDTSLISTIENYISQAIVQISNSG 120
 Qy 121 DLSGGAGLGPKFENDETAYTGSWGRPQRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Db 121 DLSGGAGLGPKFENDETAYTGSWGRPQRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Qy 241 APEIICYLOSFWMGSFILENFDSSRGKDANTLGSIHPDEAACDDSTFQCPSPRALA 300
 Db 241 APEIICYLOSFWMGSFILENFDSSRGKDANTLGSIHPDEAACDDSTFQCPSPRALA 300
 Qy 301 NHKEVUDSFRSIYIYLNGLSDSEAVAVGKYPEPTYINGNPWFCLTLAAEQLDALYQMD 360
 Db 301 NHKEVUDSFRSIYIYLNGLSDSEAVAVGKYPEPTYINGNPWFCLTLAAEQLDALYQMD 360
 Qy 361 KQGSLEVTVSLDFKKALYSDAATGTYSSSTSYISIVDAVKTFADGFSIVETHAASNG 420
 Db 361 KQGSLEVTVSLDFKKALYSDAATGTYSSSTSYISIVDAVKTFADGFSIVETHAASNG 420
 Qy 421 SMSBQYDSDGEOLSDARLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAG 480
 Db 421 SMSBQYDSDGEOLSDARLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAG 480
 Qy 481 TYSVTVTWSWPSIVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
 Db 481 TYSVTVTWSWPSIVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534

RESULT 4
 US-09-455-679-1
 ; Sequence 1, Application US/09455679
 ; Patent No. 6329186
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjarne R.
 ; APPLICANT: Svædæen, Allan
 ; APPLICANT: Bojsen, Kristian
 ; APPLICANT: Vind, Jesper
 ; APPLICANT: Pedersen, Henrik
 ; TITLE OF INVENTION: Glucoamylases with N-Terminal Extensions
 ; CURRENT APPLICATION NUMBER: 5691-200-US
 ; CURRENT FILING DATE: 1999-12-07
 ; EARLIER APPLICATION NUMBER: PA 1998 01616
 ; EARLIER FILING DATE: 1998-12-07
 ; EARLIER APPLICATION NUMBER: PA 1999 00409
 ; EARLIER FILING DATE: 1999-03-24
 ; EARLIER APPLICATION NUMBER: 60/111,674
 ; EARLIER FILING DATE: 1998-12-10
 ; EARLIER APPLICATION NUMBER: 60/126,740
 ; EARLIER FILING DATE: 1999-03-29
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
 ; US-09-455-679-1

RESULT 5
 US-09-351-814-2
 ; Sequence 2, Application US/09351814
 ; Patent No. 6352851
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjarne Roenfeldt
 ; APPLICANT: Svædæen, Allan
 ; APPLICANT: Pedersen, Henrik
 ; APPLICANT: Vind, Jesper
 ; APPLICANT: Hendriksen, Hanne Vang
 ; TITLE OF INVENTION: Glucoamylase Variants
 ; FILE REFERENCE: 5636_200-US
 ; CURRENT APPLICATION NUMBER: US/09/351,814
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: PA 1998 00937
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: PA 1998 01667
 ; EARLIER FILING DATE: 1998-12-17
 ; EARLIER APPLICATION NUMBER: 60/093,528
 ; EARLIER FILING DATE: 1998-07-21
 ; EARLIER APPLICATION NUMBER: 60/115,545
 ; EARLIER FILING DATE: 1999-01-12
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
 ; US-09-351-814-2

Query Match 100.0%; Score 2771; DB 4; Length 534;
Best Local Similarity 100.0%; **Pred.** No. 1..e-231; **Matches** 534; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;
Query 1 MSFRSLLAISGLVCTGLANVIKSRATLDSWISNEATVARTAILNNIGADGAWVSGADSGI 60
Db 1 MSFRSLLAISGLVCTGLANVIKSRATLDSWISNEATVARTAILNNIGADGAWVSGADSGI 60
Query 61 VVASPSTDNPYFYTWTRDGLVLVKTLVDFRNGDTSLSTIENYISAQIVQG1SNPSG 120
Db 61 VVASPSTDNPYFYTWTRDGLVLVKTLVDFRNGDTSLSTIENYISAQIVQG1SNPSG 120
Query 121 DLSSGAGLGEKFENDETAVGSWRQRQDGPAKATAMIGFGQMLLDNGYTSTATIW 180
Db 121 DLSSGAGLGEKFENDETAVGSWRQRQDGPAKATAMIGFGQMLLDNGYTSTATIW 180
Query 181 PLVRDLISYYAQYWNQTYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Db 181 PLVRDLISYYAQYWNQTYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Query 241 APEICLYLQSFWTGSPFLANFDSSRGKDANTLGSIHTDEAACDDSTFOPCSRALA 300
Db 241 APEICLYLQSFWTGSPFLANFDSSRGKDANTLGSIHTDEAACDDSTFOPCSRALA 300
Query 301 NHKEVVDSPRSIYTLDGLSDESEAVALGRYPEDTYNPNWFLCTLAABQLYDQW 360
Db 301 NHKEVVDSPRSIYTLDGLSDESEAVALGRYPEDTYNPNWFLCTLAABQLYDQW 360

RESULT 6
US-09-821-616-9
; Sequence 9, Application US/09821616
; Patent No. 6620324

GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Nielsen, Ruby
; APPLICANT: Leimbekk, Jan
; TITLE OF INVENTION: Thermostable Glucoamylase
; FILE REFERENCE: 5279_200-US
; CURRENT APPLICATION NUMBER: US/09/821,616
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/199,290
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 9
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; US-09-821-616-9

Query Match 100.0%; Score 2771; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-231; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDGGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDGGI 60

QY 61 WVASPSTDNPDYFYTWTDSGLVLUKJUDLFRNGDTSLISTENYISAQIYOGISINPSG 120
Db 61 WVASPSTDNPDYFYTWTDSGLVLUKJUDLFRNGDTSLISTENYISAQIYOGISINPSG 120

QY 121 DLSSGAGIGERPKFNDETAVTGSNRPDRDGPA RATAMIGFCQWLQDNGYSTATDIVW 180
Db 121 DLSSGAGIGERPKFNDETAVTGSNRPDRDGPA RATAMIGFCQWLQDNGYSTATDIVW 180

QY 181 PLVRNDLSYVAQMNQTYGLWEEVNGSSFTIAVORHALVEVEGAFA 240
Db 181 PLVRNDLSYVAQMNQTYGLWEEVNGSSFTIAVORHALVEVEGAFA 240

QY 241 APEIUCYLOSFWMCSFLANFDSSRSRGKDANTLGSINTFPEACDDSTFOPCSPRALA 300

RESULT 7
US-09-31-814-13
; Sequence 13, Application US/09351814
; Patent No. 635851

GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Roenfeldt
; APPLICANT: Svendsen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Frandsen, Torben Peter
; TITLE OF INVENTION: Glucoamylase Variants
; FILE REFERENCE: 5636_200-US
; CURRENT APPLICATION NUMBER: US/09/351,814
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: PA 1998 00337
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PA 1998 01667
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: 60/093,528
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/115,545
; EARLIER FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 13
; LENGTH: 640
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIGER
; LOCATION: (1)...(24)
; US-09-351-814-13

Query Match 99.0%; Score 2742; DB 4; Length 640;
Best Local Similarity 99.6%; Pred. No. 4.9e-229; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDGGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDGGI 60

QY 61 WVASPSTDNPDYFYTWTDSGLVLUKJUDLFRNGDTSLISTENYISAQIYOGISINPSG 120
Db 61 WVASPSTDNPDYFYTWTDSGLVLUKJUDLFRNGDTSLISTENYISAQIYOGISINPSG 120

QY 121 DLSSGAGIGERPKFNDETAVTGSNRPDRDGPA RATAMIGFCQWLQDNGYSTATDIVW 180
Db 121 DLSSGAGIGERPKFNDETAVTGSNRPDRDGPA RATAMIGFCQWLQDNGYSTATDIVW 180

QY 181 PLVRNDLSYVAQMNQTYGLWEEVNGSSFTIAVORHALVEVEGAFA 240
Db 181 PLVRNDLSYVAQMNQTYGLWEEVNGSSFTIAVORHALVEVEGAFA 240

QY 241 APEIUCYLOSFWMCSFLANFDSSRSRGKDANTLGSINTFPEACDDSTFOPCSPRALA 300

Db 241 APEILCYLQLQFWTGSFILANDPSSRGKDANTLLGSIHTFPPEAACDDSTPQCPSPRALA 300
 Qy 301 NHKEVUDSFRSYTTLNGLSSEAVNVRGVPEDTYINGNPFLCTLAAGQLYDLYQWD 360
 Db 301 NHKEVUDSFRSYTTLNGLSSEAVNVRGVPEDTYINGNPFLCTLAAGQLYDLYQWD 360
 Qy 361 KQGSLEVDVSDFFKALYSRATGYSSSTYSSIVDAVKTPADGFVSTVETHASNG 420
 Db 361 KQGSLEVDVSDFFKALYSRATGYSSSTYSSIVDAVKTPADGFVSTVETHASNG 420
 Qy 421 SMCSEQIDKSDCBQSLQASRDLTWSYAAUUTANRNRNSVUPASWGETSASSVRCAATSAIG 480
 Db 421 SMCSEQIDKSDCBQSLQASRDLTWSYAAUUTANRNRNSVUPASWGETSASSVRCAATSAIG 480
 Qy 481 TYSVVTVTSWPSIVATGGTTATPTGSGVTSKTKTATSKTSTS 530
 Db 481 TYSVVTVTSWPSIVATGGTTATPTGSGVTSKTKTATSKTSTS 530

RESULT 9
 US-09-236-063-1
 ; Sequence 1, Application US/09236063
 ; Patent No. 65337792

GENERAL INFORMATION:

- ; APPLICANT: Allen, Martin
- ; APPLICANT: Fang, Teuei-Yun
- ; APPLICANT: Li, Yuxing
- ; APPLICANT: Liu, Hsuan-Liang
- ; APPLICANT: Chen, Hui-Mei
- ; APPLICANT: Continho, Pedro
- ; APPLICANT: Hanzakor, Richard
- ; APPLICANT: Ford, Clark

TITLE OF INVENTION: PROTEIN ENGINEERING OF GLUCOMYLASE TO INCREASE PH OPTIMUM, SUBSTRATE SPECIFICITY AND THERMOSTABILITY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kohn & Associates

STREET: 30500 No. 6537792thwestern Hwy.

CITY: Farmington Hills

STATE: Michigan

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236,063

FILING DATE: CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30,955
 REFERENCE/DOCKET NUMBER: 0812.00001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 533-5050
 TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 616 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Aspergillus

Query Match 94.8%; Score 2628; DB 4; Length 616;
 Best Local Similarity 99.6%; Pred. No. 3.5e-219;

RESULT 9
 US-09-199-290-34
 ; Sequence 34, Application US/09199290
 ; Patent No. 6255084

GENERAL INFORMATION:

- ; APPLICANT: Nielsen, Bjarne R.
- ; APPLICANT: Nielsen, Ruby
- ; APPLICANT: Lehnebeck, Jan

TITLE OF INVENTION: Thermostable Glucoamylase

FILE REFERENCE: 5279-200-US

CURRENT APPLICATION NUMBER: US/09/199,290

CURRENT FILING DATE: 1998-11-24

EARLIER APPLICATION NUMBER: 1557/97

EARLIER FILING DATE: 1997-12-30

EARLIER APPLICATION NUMBER: 0925/98

EARLIER FILING DATE: 1998-07-10

EARLIER APPLICATION NUMBER: 60/070,746

EARLIER FILING DATE: 1998-01-08

EARLIER APPLICATION NUMBER: 60/094,344

EARLIER FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/979,673

EARLIER FILING DATE: 1997-11-26

EARLIER APPLICATION NUMBER: 09/107,657

EARLIER FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 34

LENGTH: 618

TYPE: PRT

ORGANISM: Talaromyces emersonii

Query Match 61.0%; Score 1689; DB 3; Length 618;
 Best Local Similarity 61.2%; Pred. No. 9.1e-138;

Query Match 94.8%; Score 2628; DB 4; Length 616;
 Best Local Similarity 99.6%; Pred. No. 3.5e-219;

Query Match 60.4%; Score 1674.5; DB 3; Length 591;
 Best Local Similarity 62.3%; Pred. No. 1.5e-136; Mismatches 314; Conservative 73; Mismatches 102; Indels 15; Gaps 3;

QY 26 TLDWSLNNEATVARTAILNNITGADGAWNSGADGIVWASPSDSTDNPYFTWTRDSGLVLK 85
 Db 4 SLDSFLATEPIALOGVNNIGPNGADVAGASAGIVVAVSPRSRSDPNFVFSWTRDAALTAK 63

QY 86 TLVDLFRNGDTSLSTENYSAQAVOGIINSPGDLSSAGLGERKFNTDETAYGSGW 145
 Db 64 YLVDAFNRRGNKDLQEQTIQOYISAQKVOTISNPGDLSTG -GLGERKFNTDETAYGSGW 122

QY 146 RPQDGPAKRAMIGFGQMLDNGYSTATDIWPLVRNLDSYVAQYWNQTYGDIWEEV 205
 Db 123 RPQDGPAKRALAYANLYLNGEASTABDIWPIVONLDSYTOYWNSTFDIWEV 182

QY 206 NGSSFTIAVORALVEGSAFATAVESCSNCSDQSAPBILCYLOSFWTGSPILANH-DSS 264
 Db 183 EGSSFFTAVQHRLAEGNALATRNLTCNSCVSOPQVLCFLOSFTWGSVLANEGGSG 242

QY 265 RSGKDANTLGSIHTDPAGECDSTFOPCSARALANKVVTDSFRSIYANSGIAEGSA 302
 Db 243 RSGKDANTLGSIHTDPAGECDSTFOPCSARALANKVVTDSFRSIYANSGIAEGSA 302

QY 325 VAVGRYPEDTYNGNPWFLCTLAEEQLYQWDQKGSLEVTVDLDFERKALYSDAAT 384
 Db 303 VAVGRYPEDVYQOGNPPYLAATAASQLYDAYQWIKIGSISITDLSLPFQDIYSAV 362

QY 385 GYSSSSSTYSVIVDAVKTFADGFVSIYETHAASNGSMSYDQKSGEOQSARDLWYS 444
 Db 363 GTYNSSSTTENDISIYAVQTYGDYVISVERKTPSGLTSQPSRDGPUSALTWYS 422

QY 445 ALLTANRNRNSVUPASWGETTASSVPGTCATSAIGYSSYTVPSPIVATGGTTAT 504
 Db 423 SLLTASARROSVUPASWGEASSSVLAVCSATSATGPYSTATNTWPS----- 470

QY 505 PTGSSVTSKTTASKTSTT 528
 Db 471 -SGSGSSTTSSAPCTPTSVAVT 493

RESULT 12

US-09-821-616-7

; Sequence 7, Application US/09821616
 ; Patent No. 6620924
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Birthe R.
 ; APPLICANT: Nielsen, Birthe R.
 ; APPLICANT: Lembeck, Jan
 ; TITLE OF INVENTION: Thermostable Glucoamylase
 ; CURRENT APPLICATION NUMBER: US/09/821,616
 ; CURRENT FILING DATE: 2001-03-29
 ; CURRENT APPLICATION NUMBER: 09/199,290
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: Talaromyces emersonii

RESULT 13

US-09-704-449-2

; Sequence 2, Application US/09704449
 ; Patent No. 6309872
 ; GENERAL INFORMATION:
 ; APPLICANT: Rey, Michael W.
 ; APPLICANT: Golightly, Elizabeth J.
 ; TITLE OF INVENTION: Polypeptides Having Glucoamylase
 ; TITLE OF INVENTION: Activity And Nucleic Acid Encoding Same
 ; FILE REFERENCE: 10101.000-US
 ; CURRENT APPLICATION NUMBER: US/09/704,449
 ; CURRENT FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 630
 ; TYPE: PRT
 ; ORGANISM: Thielavia terrestris

US-09-704-449-2

Query Match 58.3%; Score 1615.5; DB 4; Length 630;
 Best Local Similarity 58.9%; Pred. No. 2.2e-131; Mismatches 315; Conservative 83; MisMatches 112; Indels 25; Gaps 7;

QY 6 LIALSGIVCTGLANVTKRA-----TLDWSLNNEATVARTAILNNITGADGAWNSGAG 56
 Db 6 LIGLIALPAIGHFASRVRREGEVKVKSVDSFATESPIALNLICNGTGHASSV 65

QY 57 DSGIWAASPTDNPYFYTTWTRDSILVKTIVDIFRNQ-DTSLISTIENYSAQAVOGI 115

Db 66 ASGIVWASPDKTKNDYWMYPTDOSALTICKVWDPTINSDSLQAEIQYIVVIAHQLGY 125
 Qy 116 SNPGDGLSSGAGLGEKPENDEATYGSNGRPRDGPAKRTATMIGFCQWDLNGYSTA 175
 Db 126 SNPGSLSLSDGSGLGEKPENFDMSOFTGANGRPPRDGPALRAILJAYSKWLISINGYSTA 185
 Qy 176 DTIWPLVNLDSYAVQYNTQGDYLWERWNGSSPFTAQVHALVESAFATVGSSC 235
 Db 186 SSIWPKNDLAVAQ-NNTGFDLWEVEGSSPFTVANORALVEGAALATSLGTSC 243
 Qy 236 WCDSQAPELCLYQSPWFGS-FILANFDSRSKQDANTLGSHTFPBACDSTQP 293
 Db 244 ACSAVAPOLCFQFQSFWSPSGGYTAN---STARDANTLGSHTFPBAGDAATQP 299
 Qy 294 CSPRALANKEVVDSPRSIYTLDGLSDSBAVAVGRYRPEPTYNGNPWFCLTLAAEQY 353
 Db 300 CSDRALANHVKVTDAFRSYISINSGIAECSAVAVGRYRPEDSYFGGNPWFYLAELAQY 359
 Qy 354 DALYQWDKGSLTVDSDPFKALYSDATGTYSSSSSTYSSIVDAVKTADGFVSTYE 413
 Db 360 DALYWKKQGSSITVTSIAFLFKFQFSSTTPGTVSSSTYTLYNALSAVADGCMNIVA 419
 Qy 414 THAISNGSMSEQYKSDGQQLSARDLTWSYALLTANNRNSVUPASNGETASSVPGTC 473
 Db 420 YAQTGNGSSEQFSKTINGPLSAYDLTWSYAFTTAARRAGVUPPSNGAASANSVPQC 479
 Qy 474 ATSAIGTGVSSVTWSPSIVATGTTTATPTGGSVSTSKTTATAKSTST 528
 Db 480 SATSVGVSYSATATSFP-----SQTASTSAGS SPASSTATATACTSP 527

RESULT 14
 US-08-536-300A-7
 ; Sequence 7, Application US/08596300A
 ; Patent No. 5834191
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT:
 ; TITLE OF INVENTION: Production of Heterologous Peptides
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/596,300A
 ; FILING DATE: 13-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REFERENCE/DOCKET NUMBER: 26,742
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 626 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE:
 ;
 ;
 US-08-536-300A-7

RESULT 15
 US-08-536-300A-14
 ; Sequence 14, Application US/08596300A
 ; Patent No. 5834191
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT:
 ; TITLE OF INVENTION: Production of Heterologous Peptides
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/596,300A
 ; FILING DATE: 13-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REFERENCE/DOCKET NUMBER: 26,742
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 626 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE:
 ;
 ;
 US-08-536-300A-7

Query Match 56.9%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 4,8e-18;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;

Db 13 AFQAVLGPDPPLHEKRHSDDIKR-SVDSYIQETPIAQOKNLONGASCRASGAGCV 71
 Db 62 WASPSTDIDPYFVWTRISGLVVKTLVLFRING-DTSLISLTIENYIRQAIVGINSBG 120
 Db 72 VASPSKSDPDYWTWTRIALVNLIVEFTNDYNTIQTQAYAJAQAKLQGVNSBG 131
 Db 121 DUSSGAGI-GEKPENDEATYGSNGRPRDGPAKRTATMIGFCQWDLNGYSTATDW 180
 Db 132 SLNGAGI-GEKPENDEATYGSNGRPRDGPAKRTATMIGFCQWDLNGYSTATDW 191
 Db 181 PLVRNDLSYVAQWQNQTYDLMWEVNGSSFTIAASHRVLVGSAPAVGSSCSWDSQ 240
 Db 192 PIYKNDIAYTAQWQNQTYDLMWEVNGSSFTIAASHRVLVGSAPAVGSSCSWDSQ 251
 Db 241 APEIICLYQSPWFGS-FILANFDSRSKQDANTLGSHTFPBACDSTFOPCSPRL 299
 Db 252 APOLCFRCQFOSFWNSGTYLISNFYRSDKINDVLSHTFPBACDSTFOPCSPRL 311
 Db 300 ANHKEVWUSFRSIVTLDGLSDSEAVAVGRYRPEPTYNGNPWFCLTLAAEQYDALYQW 359
 Db 312 ANHKWVUDSMR-FWGVNNGRFTAGKAAYAVGRYADVYQYNGNPWFYLAELAQYVW 370
 Db 360 DKQGSLETDVSDPFKALYSDATGTYSSSSSTYSSIVDAVKTADGFVSTFPBACDSTFOPCSPRL 419
 Db 371 KKQGSITITSLAFLKQVPSVSTGTYSSSSSTYTAIINVITYAQGFDIVAQYVPSD 430
 Db 420 GSMEQYKSDGQQLSARDLTWSYALLTANNRNSVUPASNGETSSASSVPGTCATSAI 479
 Db 431 GSIAEQPKDGSQPLSATHLTWSYASFFSAAARRAGVUPPSNGAASANLSPGSCASTVA 490
 Db 480 GTYSSVTWSPSIVATGTTT-ATPTGGS---VTSKTTATAKST 524
 Db 491 GSYATATATSFPANLTPASTVTPPTQGCAADHEVLNTFNEKVTSYQGOT 541

;
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 626 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE:
 ; US-08-596-300A-14

Query Match 56.9%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 4.8e-128; Gaps 6;
 Matches 306; Conservative 85; Mismatches 130; Indels 10;

```

QY 2 SPRSLALSGIVCTGLANLSSRATLDSWLSNEATPARTATLNNIGADGAWSGADSGIV 61
Db 13 AFQAVLGLPDPDIHEKRHSIDIKR-SDSDYIQTETPTAQKNLICNIGSGCERASGAAGVV 71
Qy 62 VASPSTNDPFDYTWTRDSGVLTKLVDLFENG-DISLSLSTENYISAQATVOGINSNPG 120
Db 72 VASPKSKSPDYTWTRDAALVTKLIVDEFNDNTLQNTTOAYAAQAKLQGVSNPSG 131
Qy 121 DLSSGAGLGERKFNVEATAYTGSWGPQRDGPALARATAMIGFGQWLDNGYTSTATDIW 180
Db 132 SLSNGAGLGERKFMDLQDFPGRQDPPRLAIALIGYKWIUSNGADTAKSIIW 191
Qy 181 PLVRNDLISYYAQYWNQTYGDWEEWNGSSEFTIAVORHALTEGSAFATAVGSSCSWCDSQ 240
Db 192 PIVKNDIAYTQYIWNNTGFDIWEVNSSSFPTIAASHRALVEGSAKSVSSCSDAI 251
Qy 241 APEILLYQLOSMWTGFS-FLIANFDSSRSQKDANTLGSISHTDPPEACDDSTFQPSPRAL 299
Db 252 APOILCPQOSHWSNSNGYIISHPNVNYSRGKDINSVLTSHNFDPAAGCDVNTFQPCSDRAL 311
Qy 300 ANHKEVUDSFHSITYTLANDGLSDEAVALGVPEDTYINGNPWFCLIAAEQLYDIALW 359
Db 312 ANHKVUVDSMR-FWGUNSGRAKGAAAVGRRAEDVYNGNWYLATLAABOLYDVW 370
Qy 360 DKQGSLEVTDVSLDFKALYSDAATGTYSSSSSTVSSIIVDAVKTFADGFYVSIVETHASN 419
Db 371 KKQGSITVTSSLAFFKDLVSVSITGYTSSSSSTYTAIINATTIADGFVDIVAQTPSD 430
Qy 420 GSMSEGYDKSGEQLSARDLWSYAALLTANRNSWVPAWGETSASSVPGTCATSAI 479
Db 431 GSIAEOPDKDQGAPLSATHLWMSYASPLSAAARRAGIVUPRSGAASANSLGSCASTVA 490
Qy 480 GTYSSTVTSPSPSIATGGTTT-ATPTGSS----VTSTSXTTASKT 524
Db 491 GSYATATATSPANLTPASTTVTPPPQRTGCAADHEVLTIFNEKVITSYGQT 541
  
```

Search completed: June 17, 2004, 17:48:36
 Job time : 25 SECs

HIS PAGE LEFT BLANK

Copyright (c) 1993 - 2004 GenCore version 5.1.6 Compugen Ltd.

OM protein - protein search, using SW model

Run on:

June 17, 2004, 17:42:38 ; Search time 46 Seconds

(without alignments)

3662.755 Million cell updates/sec

Title: US-10-038-723-2

Perfect score: 2771

Sequence: 1 MSFRSLALSLGLVCTGIANV.....SKRTATASKTSTTRSCMSL 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	2669.5	95.3	639	3	Q870GB	0870GB aspergillus
2	2564.5	92.5	639	3	Q12537	Q12537 aspergillus
3	1689	61.0	618	3	Q9CIV4	Q9CIV4 talaromycetes
4	1518	54.8	493	3	Q59846	Q59846 aspergillus
5	1400	50.5	620	3	Q12623	Q12623 humicola gr
6	1394	50.3	579	3	Q12596	Q12596 corticium r
7	1286	46.4	571	3	Q9P4C5	Q9P4C5 lentinula e
8	784	28.3	609	3	Q8J0PB	Q8J0PB mucor circi
9	728	26.3	579	3	Q7ZKX9	Q7ZKX9 rhizopus or
10	674	24.3	515	3	Q8TFE5	Q8TFE5 baccharomyces
11	187	6.7	599	17	Q96210	Q96210 bullulobus
12	185.5	6.7	636	17	Q9HLB8	Q9HLB8 thermophilic
13	181	6.5	1588	16	Q8XDG4	Q8XDG4 escherichia
14	174.5	6.3	1236	3	Q9C105	Q9C105 schizophyllum
15	174.5	6.3	659	17	Q97B07	Q97B07 thermophilic
16	174.5	6.3	990	16	Q83J22	Q83J22 shigella f1

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

SPREMBI_25 :*

- 1: bp_archea:*
- 2: bp_bacteria:*
- 3: bp_fungi:*
- 4: bp_human:*
- 5: bp_invertebrate:*
- 6: bp_mammal:*
- 7: bp_micr:*
- 8: bp_organelle:*
- 9: bp_phage:*
- 10: bp_plant:*
- 11: bp_Rodent:*
- 12: bp_virus:*
- 13: sp_Vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database :

DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008938; Glyco_trans_6hp.
 DR Pfam; PF00686; CBM 2.0; 1.
 DR PRINTS; PR00736; GLYHYDROLASE15.
 DR PIRSF; PIRSF01031; GLN-a-glcid SBD; 1.
 SQ SEQUENCE 639 AA; 68308 MW; 025AD856B6542B69 CRC64;
 Query Match 95.3%; Score 2659.5; DB 3; Length 639;
 Best Local Similarity 98.1%; Pred. No. 3.96-162; Mismatches 6; Indels 3; Gaps 3;
 Matches 541; Conservative 1; MisMatches 6; Del 1; Insert 1; Signal 1; FT 24
 QY 1 MSFRSLLAISGLVCTGLANVISKRATDWSLNEATVARTAILNNIGADGAWSGADSGI 60
 Db 1 MSFRSLLAISGLVCTGLANVISKRATDWSLNEATVARTAILNNIGADGAWSGADSGI 60
 QY 61 VVASPSTNDPYFTWTDGLVLUKTLVLDLFRNGDTSLSLTENYISQAIVQGISNSG 120
 121 DLSSGAGLGEPKENDEAYTGSGRPQDGALRATAMIGFGQWLNGYTSTATDVW 180
 61 VVASPSTNDPYFTWTDGLVLUKTLVLDLFRNGDTSLSLTENYISQAIVQGISNSG 120
 Db 121 DLSSGAGLGEPKENDEAYTGSGRPQDGALRATAMIGFGQWLNGYTSTATDVW 180
 181 PLVRNDLSVQAQMNQTGDWEEVNGSSFTAVQRALVEGSAFATAVGSSCSWCDSQ 240
 181 PLVRNDLSVQAQMNQTGDW-EVNGSSFTAVQRALVEGSAFATAVGSSCSWCDSQ 239
 QY 241 APETILCYQSFWTCSFFILANFDSSRSRGKANT-LIGSHTFPDRAACDSTSOPCSPRAL 299
 240 APETILCYQSFWTCSFFILANFDSSRSRGKANT-LIGSHTFPDRAACDSTSOPCSPRAL 299
 QY 300 ANHKEVWPSRIFTYLTNDGNSDSEAVALGRPEPTYYNCPWFCLTAAEQLDALYQW 359
 300 ANHKEVWPSRIFTYLTNDGNSDSEAVALGRPEPTYYNCPWFCLTAAEQLDALYQW 359
 Db 360 DKQGSLEVTDSLDPFKALYSDAATGTSSSSSTSYTDAVKTFADGVSVTEHAASN 419
 360 DKQGSLEVTDSLDPFKALYSDAATGTSSSSSTSYTDAVKTFADGVSVTEHAASN 418
 QY 420 GSMSBQYDKSDGEOLSDARDLTWSVALLTANNRNSVVASWGSTSASSVPGCAATR1 479
 419 GSMSBQYDKSDGEOLSDARDLTWSVALLTANNRNSVVASWGSTSASSVPGCAATR1 478
 Qy 480 GTTSSVTWPSLVATGGTTTATPTGGSVTSTSKTATASKTSTRS 530
 479 GTTSSVTWPSLVATGGTTTATPTGGSVTSTSKTATASKTSTRS 529
 RESULT 2
 Q12537 ID Q12537 PRELIMINARY; PRT; 639 AA.
 AC DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Glucosaminylase precursor (EC 3.2.1.3).
 GN GLA.
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitobporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=10531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X-100;
 RA Diagne I., Pechexonov V.T., Bulat S.A., Fisrov L.M.;
 RT "A glucosaminylase gene from Aspergillus awamori X-100: structure,
 allocation, and gene phylogeny";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; US9303; AAB02927.1; -.
 DR HSPR; P0464; 1GAI.
 GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR Pfam; PF005376; R:polysaccharide metabolism; IEA.
 DR InterPro; IPR0244; CBD 4.
 DR InterPro; IPR002448; EF-hand.
 DR PIRSF; PIRSF01031; GLN-a-glcid SBD.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008938; Glyco_trans_6hp.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR PRINTS; PR00736; GLYHYDROLASE15.
 DR PIRSF; PIRSF01031; GLN-a-glcid SBD.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008938; Glyco_trans_6hp.
 DR Pfam; PF00686; CBM 2.0; 1.
 DR PRINTS; PR00736; GLYHYDROLASE15.
 DR PRODOM; PD001568; CBD 4; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00820; GLUCOAMYLASE; 1.
 DR PIRSF; PIRSF01031; Glu-a-glcid SBD; 1.
 KW Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 PT CHAIN 25 639 GLUCOAMYLASE.
 SQ SEQUENCE 639 AA; 68277 MW; 6F93D0637D174ACB CRC64;
 QY 1 MSFRSLLAISGLVCTGLANVISKRATDWSLNEATVARTAILNNIGADGAWSGADSGI 60
 Db 1 MSFRSLLAISGLVCTGLANVISKRATDWSLNEATVARTAILNNIGADGAWSGADSGI 60
 QY 61 VVASPSTNDPYFTWTDGLVLUKTLVLDLFRNGDTSLSLTENYISQAIVQGISNSG 120
 121 DLSSGAGLGEPKENDEAYTGSGRPQDGALRATAMIGFGQWLNGYTSTATDVW 180
 61 VVASPSTNDPYFTWTDGLVLUKTLVLDLFRNGDTSLSLTENYISQAIVQGISNSG 120
 Db 121 DLSSGAGLGEPKENDEAYTGSGRPQDGALRATAMIGFGQWLNGYTSTATDVW 180
 181 PLVRNDLSVQAQMNQTGDWEEVNGSSFTAVQRALVEGSAFATAVGSSCSWCDSQ 240
 180 PLVRNDLSVQAQMNQTGDW-EVNGSSFTAVQRALVEGSAFATAVGSSCSWCDSQ 239
 QY 241 APETILCYQSF----WTGSFFILANFD---KDINTLGSHTFPDRAACDSTSOPC 295
 240 APETILCYQSFSSRSRGKANT-LIGSHTFPDRAACDSTSOPC 294
 Db 296 PRALANHKEVWPSRIFTYLTNDGNSDSEAVALGRPEPTYYNCPWFCLTAAEQLDA 355
 295 PRALANHKEVWPSRIFTYLTNDGNSDSEAVALGRPEPTYYNCPWFCLTAAEQLDA 354
 QY 356 LXQMDKQSLLEVTDSLDPFKALYSDAATGTSSSSSTSYTDAVKTFADGVSVTEH 415
 355 LYQMDKQSLLEVTDSLDPFKALYSDAATGTSSSSSTSYTDAVKTFADGVSVTEH 414
 Db 416 AASNGSMSBQYDKSDGEOLSDARDLTWSVALLTANNRNSVVASWGSTSASSVPGCA 475
 415 AASNGSMSBQYDKSDGEOLSDARDLTWSVALLTANNRNSVVASWGSTSASSVPGCA 474
 QY 476 TAAIGTYSSVTWPSLVATGGTTTATPTGGSVTSTSKTATASKTSTRS 530
 475 TAAIGTYSSVTWPSLVATGGTTTATPTGGSVTSTSKTATASKTSTRS 529
 RESULT 3
 Q9C1V4 ID Q9C1V4 PRELIMINARY; PRT; 618 AA.
 AC Q9C1V4; DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Glucosaminylase precursor (EC 3.2.1.3).
 GN GA.
 OS Talaromyces emersonii.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Talaromyces.

OX NCBI_TaxID=68825;
RN [1]
RP SEQUENCE FROM N.A.
RA Nielsen B.R., Lehmbbeck J., Frandsen T.P.;
RT "Cloning, heterologous expression, and enzymatic characterization of a
thermostable glucosidase from *Talaromyces emersonii*";
RL Submitted (DEC-2000) to the EMBL/Genbank/DDBJ databases.
DR EMBL; AJ314803; CAC28076.1; --.
DR HSSP; P0464; ICA1.
GO; GO:004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0016796; P:polysaccharide metabolism; IEA.
DR IntePro; IPR002044; CBD_4.
DR InterPro; IPR00291; Gluta-glcid_SBD.
DR IntePro; IPR00165; Glyco_hydro_15.
DR IntePro; IPR008928; Glyco_trans_6hp.
PFam; PF00686; CBM_20_1.
DR PFam; PF00686; CBM_20_1.
DR PRINTS; PRO0736; GLUDRILASE15.
DR PRODom; PS001568; CBD_4; 1.
DR PIRSF; PIRN00131; Glu-a-glcid_SBD; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 20 . POTENTIAL.
FT CHAIN 28 618 GLUCOAMYLASE.
SQ SEQUENCE 618 AA; 65429 MW; C48A034AZC06E5B2 CRC64;
Query Match Best Local Similarity 61.0%; Score 1689; DB 3; Length 618;
Matches 322; Conservative 75; Mismatches 111; Indels 18; Gaps 5;
QY 7 LALSGLUVCTGLANV-ISKRAI-LDSWLSNEAVARTAILNNIGADGAWAGADSGIVWA 63
9 ICLIGLUPPAAFARAPVAAVARAGCSDLSLATEPIALOGVUNNIGPNAVGAGASAGIVWA 68
QY 64 PSTNDNPDYFVWTRDGSGLVLUKTLVDFRNPGTSLISTENVTISAOVQDISNPSGDLIS 123
69 SPSRSRDPNYYFSWTRDHALTAKVLVRFAIGNSKDELOTIQVISAQKVQTISNPSGDLIS 128
124 SGAGLGPBPKFENYDETAATYGSGSRPQDGPARATAMMGFCGWLDDNGYTSTADTVMPV 183
129 TG-GLGEPBKPNVNETAFTGPMCRPQDGPAKLRATAIAYANLYLIDNEASTADEIIWPIV 187
QY 184 RNDLISVVAQYMQNTGDIWEEUNGSSPFTIAVORHALVEAGSAPATAVGSSCSWCDQAPE 243
188 QNDLISVITQVNNSSTEFLWEVEGGSPFTTAVOHRALVEAGNALATRNLHICNSQVQ 247
Db 244 ILCYQSFWTSFILANP-DSSRGKDANTLGSIHFPDPBAACDSTFQPCSPRALAHN 302
248 VLCFPLQSYWTSVYVIANFGGSQRSGKDVNVSITLGSIHFPDPAGCDSTFQPCSARALAHN 307
303 KEWDSRFSRIFTYLTNDGSDSEAVAVERYPEDTYNYNGNPWFCTLAEAQQLDALYQDKO 362
308 KVVTDSFRSIVAINSGIAEGSAAVAVGRYPELVDYQGENPWPWYIATAAAEQLDIAQWKKI 367
QY 363 GSLEVTDVSLPFKALYSDAATGTYKSSSSYTSITDAVKTFADGVSIUETHAASNGSM 422
368 GSISITDVSLLPFQDITPSAAGVGTNNSGTFENDIISAVQYQGDGLIVEKYTPDGSGL 427
Db 423 SBOYDKSDGEQSLSARDITWSAALLTANRNRNSVVPASWGETSASSVPGTCAATSALGY 482
428 TEQFSRRTDGTISASALTWSASLITASRAROSVVPASWGEASSVPAVQCSATSATGPY 487
QY 483 SVTVTWSWPSIUTATGGTTT-TPTGGSVTSKTATASCTSTT 528
Db 488 STATNTWVPS-----SGSCSSTT'SABCTPTPSVAVT 520
RESULT 4 PRELIMINARY; PRT; 493 AA.
ID 059846
AC 059846; 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)

01-OCT-2003 (T-EMBLrel. 25, last annotation update)
DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
DE Glucosidase.
OS Aspergillus oryzae.
OC Eurotiomycetes; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OK NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O-013;
RX MEDLINE=98172744; PubMed=9511753;
RA Hata Y., Ishida H., Ichihara E., Kawato A., Sugiyama K., Inayasu S.;
RT "Nucleotide sequence of an alternative glucosidase-encoding gene
(glab1) expressed in solid-state culture of *Aspergillus oryzae*.";
RL Gene 207:127-134(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O-013;
RA Hata Y., Ishida H., Kojima Y., Ishikawa E., Kawato A., Sugiyama K.,
RA Inayasu S.;
RT "Comparison of two glucosidases produced by *Aspergillus oryzae* in
RT solid-state (koji) and in submerged culture.";
RL J. Ferment. Bioeng. 84:52-53(1997).
DR EMBL; AB007825; BAM25205.1; --.
DR PIR; PC6503; JC6538.
DR PROSITE; PS00820; GLUCOAMYLASE; 1.
DR PRINTS; PRO0736; GLUDRILASE15.
SQ SEQUENCE 493 AA; 52401 MW; 3707B3A6F0C66256 CRC64;
Query Match Best Local Similarity 54.8%; Score 1518; DB 3; Length 493;
Matches 280; Conservative 82; Mismatches 123; Indels 2; Gaps 2;
QY 5 SLAISGLUVCTGLANVSKRATDLSMSNEAVARTAILNNIGAGMAGWAGADSGIVWA 64
8 SINATAGAVAHPSFPKIKROSDLNAPIEACTPIQOGVUNNIGPNAVGAGIVWA 67
Db 65 PSTNDNPDYFVWTRDGSGLVLUKTLVDFRNPGTSLISTENVTISAOVQDISNPSGDLIS 124
68 PSKSNDPDYFVWTRDGSGLTMEVIRQFQGDTATLSITQVYDQSANEQAVSNPQGGLSD 127
Db 125 GAGLGPBPKFENYDETAATYGSGSRPQDGPAKLRATAIAYANLYLIDNEASTADEIIWPIV 184
128 GSGLAEPKFYINISQFDSWKRPODGPAKLRASALIAYAGLSSLISSDKQSVKANIWPIVQ 187
QY 185 NDLSVVAQYMQNTGDIWEEUNGSSPFTIAVORHALVEAGSAPATAVGSSCSWCDQAPEI 244
188 NDLSVVAQYMQNTGDIWEEUNGSSPFTIAVORHALVEAGSAPATAVGSSCSWCDQAPEI 246
Db 245 ILCYQSFWTSFILANP-DSSRGKDANTLGSIHFPDPBAACDSTFQPCSPRALAHN 303
247 LCHLQDFWNSAVLSPLPTNGSGDTSNLISHTFDPAAACDSTFQPCSPRALAHN 306
QY 304 EVDSSRFSRIFTYLTNDGSDSEAVAVERYPEDTYNYNGNPWFCTLAEAQQLDALYQDKO 363
307 LVVDSRFSRIFTYLTNDGSDSEAVAVERYPEDTYNYNGNPWFCTLAEAQQLDALYQDKO 366
QY 364 SLEVDVSLPFKALYSDAATGTYKSSSSYTSITDAVKTFADGVSIUETHAASNGSM 423
Db 367 QVNVTTSLPPFKDLSNVNTGYSVAKSSAVESLTSVAKHYADGFTSVVQBYTPDGGALA 426
QY 424 EQYDKSDGEQSLSARDITWSAALLTANRNRNSVVPASWGETSASSVPGTCAATSALGY 483
Db 427 EQYRSRQGTPVVASDLTWYAAFLSAVGRNGTVPASWGSASSVPAVQCSATSATGPY 486
QY 484 SVTVTWSW 490
Db 487 TPTVGSW 493

QY	299 LANHKENDVDSRFSIYTIVLNDGSDSEA VAVGRYPEDTYNGNWFICLAAJAEQLYALYQ	358 WKAAGEELAVTYSVSLAFFQFQDSSITAGTYAASSSSVVTISLSDIQAFADFDIVAKTPS	Db	193 TVDLWBEIYSSFFESTVAOHLARQCTLSRAIGONSLASSYGNORDPLCFLQSYNPT	252
Db	298 LANLKVVUDSFSSITYTINSGSISSTGATGRPEPDSTYNGNWFICLAAJAEQLYALIV	419 NCSMSEDYDKSUGEQLSARDLWSYALLTANRNRNSVIPSWSGER-SASSPGTCAT-AT	Db	253 G-YMTANTGGRSGDANSVLSASINHPTDAAGCATTQFQSDVVALNLFYVNAFRAY	313
QY	359 WIKQGSLEVTDVSLDFKALYSDAATOTYSASSSTYSSIVIAVVKTRADGFESIVERTHAS	418 SQFLSEQYDKSAGQDAANLWYSAAITAQOARNQFTGASWG--AKGYSTSCSTGAT	Db	253 G-YMTANTGGRSGDANSVLSASINHPTDAAGCATTQFQSDVVALNLFYVNAFRAY	311
Db	358 WKAAGEELAVTYSVSLAFFQFQDSSITAGTYAASSSSVVTISLSDIQAFADFDIVAKTPS	419 NCSMSEDYDKSUGEQLSARDLWSYALLTANRNRNSVIPSWSGER-SASSPGTCAT-AT	Db	253 G-YMTANTGGRSGDANSVLSASINHPTDAAGCATTQFQSDVVALNLFYVNAFRAY	317
QY	419 NCSMSEDYDKSUGEQLSARDLWSYALLTANRNRNSVIPSWSGER-SASSPGTCAT-AT	418 SQFLSEQYDKSAGQDAANLWYSAAITAQOARNQFTGASWG--AKGYSTSCSTGAT	Db	314 TLNDGLSDSEA VAVGRYPEDTYNGNWFICLAAJAEQLYALYQKQSESLEVTVSLD	373
Db	418 SQFLSEQYDKSAGQDAANLWYSAAITAQOARNQFTGASWG--AKGYSTSCSTGAT	477 SAIGTIVSSVVT-----SNPSIVATG----GTTTAT-----PTGSSGVST	Db	312 EINSGISTNEAVLTGRGPEDVYMGNSFWYLTLAVAEQLYDSLIVNSQSSLDVNTISLP	371
QY	477 SAIGTIVSSVVT-----SNPSIVATG----GTTTAT-----PTGSSGVST	475 SPGGSSOSVEVTFDWWATTIVQGQNIYTGDSSELGNWTANGVALSSANYPIWSATIALP	Db	374 FPKALYSDAATCTYSSSSVTSVDAWKTRADGEVISVERHAASMSMSQYDSDGQ	433
Db	475 SPGGSSOSVEVTFDWWATTIVQGQNIYTGDSSELGNWTANGVALSSANYPIWSATIALP	515 SKT-----ATASKSTTRSG 531	Db	372 FPKQFDTTITAGTYTSSPSRFSTLTAAVKTFSDFEVALKVTPSSGGLAEOISRGAP	431
QY	515 SKT-----ATASKSTTRSG 531	535 ADTIQKVNVIDGSTVIWEDAISNRBTTPASG 568	Db	434 LSARDITWSYALLTANRNRNSVIPSWSGER-SASSPGTCAT-AT	471
Db	535 ADTIQKVNVIDGSTVIWEDAISNRBTTPASG 568	515 --KTRTASKSTT 527	Db	432 VSAVDITWSYASALTEDARAGVIRCGWSQAGLSNCGGVVAQAVSFTVNDASTLEQ	491
RESULT 7	Q9P4C5 PRELIMINARY; PRT; 571 AA.	Q9P4C5; 01-OCT-2000 (T-EMBL; 15, Created)	Db	492 NVLTGAVDALEWDSTDNAILLSSANYPTWSVTVDLPGSTDVQKYKIKKOGSGIVIWE SD 551	552
Q9P4C5	PRELIMINARY; PRT; 571 AA.	ID DT	516 --KTRTASKSTT 527	QY	472 --TCAATSAIGT-----SSVMTWSPIVATG----ATPTCGSGSVSTS- 515
AC	09P4C5; 01-OCT-2000 (T-EMBL; 15, Last sequence update)	AC ID	552 PNMEITTPANGTYAT 566	Db	492 NVLTGAVDALEWDSTDNAILLSSANYPTWSVTVDLPGSTDVQKYKIKKOGSGIVIWE SD 551
ID	09P4C5; 01-OCT-2003 (T-EMBL; 25, Last annotation update)	AC ID	516 --KTRTASKSTT 527	QY	472 --TCAATSAIGT-----SSVMTWSPIVATG----ATPTCGSGSVSTS- 515
DT	01-OCT-2003 (T-EMBL; 25, Last annotation update)	AC ID	552 PNMEITTPANGTYAT 566	Db	492 NVLTGAVDALEWDSTDNAILLSSANYPTWSVTVDLPGSTDVQKYKIKKOGSGIVIWE SD 551
RN	[1]	SEQUENCE FROM N.A.	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
RP	Lentinula edodes (Shitake mushroom) (Lentinus edodes)	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
QX	Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
OC	Agaricales; Tricholomataceae; Lentinula.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
OX	NCBI_TaxID=535;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DE	Glucosidase.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
RA	Lentinula edodes (Shitake mushroom) (Lentinus edodes)	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
RA	Zhao J., Chen Y.H., Kwan H.S.; Characterization, and Differential Expression of a Glucosidase Gene from the Basidiomycetous Fungus Lentinula edodes.;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
RT	"Molecular Cloning, Characterization, and Differential Expression of a Glucosidase Gene from the Basidiomycetous Fungus Lentinula edodes.";	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
RL	Appl. Environ. Microbiol. 66:2531-2535(2000).	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	EMBL; AF20541; AAF5523.1; -.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	HSSP; P0464; 1GA1.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	GO; GO:0003824; F: catalytic activity; IEA.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	GO; GO:0005976; P:polysaccharide metabolism; IEA.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	NCBI_TaxID=36080;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	[1]	SEQUENCE FROM N.A.	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Rouholt Larsen J., Pedersen P.A.; Hougstedt-Larsen J., Pedersen P.A.;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	EMBL; AY169303; AAB85205.1; -.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Mucor circinelloides.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Glucosidase GLAM.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Mucor circinelloides.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Glucosidase GLAM.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Glucosidase GLAM.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	InterPro; IPR008928; Glyco_trans_6hp.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Pfam; PF00686; CBM_20_1.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	PRINTS; PR00736; Glyco_hydro_15_1.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	PRODOM; PRO00168; CBM_4_1.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	DR; PROSITE; PS00820; GLYCOHYDRASE15.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	DR; PROSITE; PS00820; GLYCOHYDRASE15.	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	SEQUENCE 571 AA; 6161 MW; AIBDIECC448E97FP CRC64;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	Query Match 46.4%; Score 1286; DB 3; Length 571; Best Local Similarity 47.9%; Pred. No. 6.7e-74; Matches 266; Conservative 91; Mismatches 150; Indels 48; Gaps 10;	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	19 NIVSKRATDLSLNSNEATVARTAILNNGIDGAWVGADSGTIVASPASTNDPYFTWTR 78	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	14 SVWAQSSVIDAVVASESPIAKRASMLANGIPKGSKSSGAFVIAVSPTEPDYLTWTR 73	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	79 DSGGLVLUKLVLDFRNG-DTSILSTIENYISAQATVQGTSNPGDLSGGAGLGEPEKRNDE 137	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	74 DSALTPOTIIQFOFTLGDTTIAEIDYVQGQAIQVQIPNPGDITG-GIGEPKRYNE 132	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	138 TAYTGSGWRPDRGPALARATMIGFGCWLNGYTFATDIPWPLYRNDLSYQAQYNNQTYGD 197	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	133 TAFTGPWGRPDRGPALARSTLTWNLVYLLSBNFTPVTDIWPITENDLNLYVSSWNQS 192	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	198 GYDLWEEVNGSSFFTIAVQHRLAVEGSAFATAVG--SSCSNCDSQAPBILCYLQSFN--T 253	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB
DR	201 LWEENVNGSSFFTIAVQHRLAVEGSAFATAVG--CSWCDSQAPBILCYLQSFN--T 253	Q8J0PB; 01-OCT-2003 (T-EMBL; 23, Last sequence update)	Q8J0PB	Q8J0PB PRELIMINARY; PRT; 609 AA.	Q8J0PB

QY 394 VSVIVDAVKTFRDGFSIVSIVEHTHAASNSMSQYDKDGEQISARDLTWSYALITANRR 453
|::|::|::|::|:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
Db 449 VKVVKILQRDSFLKVLHIDNGQLTBIRYTGFOAGAVSLTWSSGSLSLNAR 508
|:|:
QY 454 NSVW 457
|:
Db 509 NGLI 512
|:
RESULT 11
Q96210 PRELIMINARY; PRT; 599 AA.
ID Q96210
AC 096210;
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Hypothetical protein ST2017.
GN ST2017.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Ox Sulfolobus;
NCBI_TaxId=11955;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosegi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshiawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
RA Oshimi T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
EMBL: AP000988; BAB#7116:1; -
DR GO; GO_0016020; C:membrane; IEA.
DR GO; GO_0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR GO; GO_0005215; F:transporter activity; IEA.
DR GO; GO_0005976; P:polysaccharide metabolism; IEA.
DR GO; GO_0006810; P:transport; IEA.
DR InterPro; IPR00165; Glyco_hydro_15.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00723; Glyco_hydro_15_1.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00723; Glyco_trans_6hp.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00723; Glyco_hydro_15_1.
DR InterPro; IPR000531; TonB_DEPENDENT_RBC_1; 1.
KW Hypothetical protein; Complete proteome;
SQ SEQUENCE 599 AA; 69661 MW; F8B94CAE7731D119 CRC64;
Query Match 6.7%; Score 187; DB 17; Length 599;
Best Local Similarity 22.3%; Pred. No. 0.001; Gaps 23;
Matches 102; Conservative 58; Mismatches 151; Indels 146; Gaps 23;
QY 29 SWL---SNEATVARYAIL---NNIGADCAWGSAGSDGIVVASPSTDNPDXWTWR 78
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 235 AWLVKARDYDVPSRSLLIHHAWHORN---GALPRAALDTDMRNDT---YNYVWHR 286
|:|:
QY 79 DSGGLVLTLDLFRNGDTSLSLTIENVIYISAQAIVGISINSSGDLSGGAGIGGPKEVNDET 138
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 287 DAAF-----ASIALITYGV---QDPIRNLNFPTKPLPNGFDFQ-KTCDF-- 327
|:|:
QY 139 AYTGSWGRP-----ORDGPALRATMIGFGOWLNGYSTATIIVWPLVRNDL 187
|:|:
Db 328 ---GNWGSTWHFWPNRPSIPIQED----ETALMLYALWHRHSRFD--IDFVRPLYAPFV 377
|:|:
QY 188 SYVAQOW-----NQCG-----YDLMREWNSSSPFTIAVQHARHALVEGSAFATAVGSSCSWCDSQAPELICYLQSFWTGFSILANFDSS 237
|:|:
Db 378 RKKIAEFLVLSYRDTEFLGPLPLRSYDLMWERLGHFTFSLAVVAGLMSAYKFABPFGE-NLK 436
|:|:
QY 238 D---SQAPEIICYLQOSFWTGS-FILANFDSSRSKG---DANTLILGSIHTFDEAACDSTF 291
|:|:
Db 437 DKLTAANEVEVKGLERFYVGDHFARTIYEDNSIDKTVDASTLFASIL-----GPF 486
|:|:
RESULT 12
Q9HL88 PRELIMINARY; PRT; 636 AA.
ID Q9HL88
AC Q9HL88;
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE Hypothetical protein Ta0342.
GN TA0342.
OS Thermoplasma acidophilum.
OC Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
NCBI_TaxId=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1778;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
acidophilum.;"
RL Nature 407:503-513(2000).
DR EMBL: AL44506; CACT1486.1; -
DR GO; GO_0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR GO; GO_0005976; P:polysaccharide metabolism; IEA.
DR InterPro; IPR00165; Glyco_hydro_15.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00723; Glyco_hydro_15_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 636 AA; 73269 MW; FFA46856CCDSE9AFD CRC64;
Query Match 6.7%; Score 185.5; DB 17; Length 636;
Best Local Similarity 19.0%; Pred. No. 0.0014; Gaps 15;
Matches 86; Conservative 56; Mismatches 139; Indels 171; Gaps 15;
QY 57 DSGIVVASPSTD----NPDXWTWRDSLGIKVLTKLUDPFRNGDTS-LISTIENVIYSAQ 109
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 281 DLGATASCDSDILKLSHDGYVWPRDASMAVAL-STSGHSETARRFFPALMEDSSEE 339
QY 110 AIVOGINSNPGDLSSGAGIGGPKEVNDETAYTGSGWGRPDRGPAI---RATAMIGFGQ 164
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 340 GYLYHKVNVGKIAS-----SMLPHVNGKSYPPGDETAIVWVAL 381
QY 165 WLDNGTYSTADIVWPLVRNDLVSQAYQMN-----QTYGDWEE 204
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 382 WEYFK-----NDIGTAPYXERLITRADEPMTNFVDNGNLUKPKEFDFD 428
|:|:
QY 205 VNGSSFTIAVQHARHALVEGSAFATAVGSSCSWCDSQAPELICYLQSFWTGFSILANFDSS 264
|:|:
Db 429 RYGHAYTVAIVVAAKKAASNFANVFG-----DPP 458
|:|:
QY 265 RSKDQANTLGSIHTPDRBACDSTFOPCSPRALANHKE--VYDSFSRISIYTLDGLSPS 322
|:|:
Db 459 LSEKVTENAAERMYHAFDERPYSEDIGY---ARAIIDKGPDFTDVSLTSLSLV-FGMKDA 514
|:|:
QY 323 E-----AVAVGPRYPEDTYN-----GIPWFELTAAEBOYVA 355
|:|:
Db 515 DDPKVISTMORISEDlwWnvgGgTaryQndrYMKDDSDSVPGbWPWITlWma-RYMR 573
|:|:

Query Match 6.3%; Score 175; DB 3; Length 1236;
 Best Local Similarity 21.5%; Pred. No. 0.016;
 Matches 129; Conservative 91; Mismatches 242; Indels 138; Gaps 21;

DR InterPro; IPR008928; Glyco_trans_hph.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 KW Complete proteome.
 SQ SEQUENCE 659 AA; 76598 MW; 36101F

5405F13B33 CRC64;

QY	10	SGUVCGLANVSKRATLDSMLSNEATVARTAILNIGAD-----
Db	528	SSITSPMTSVLSSSSSIPTSSSDFSSSITISSG1SSSSIPSTFSSVSSILSSSTSSP 587
QY	50	--GAWTGADGIVASPASTNDPDIYFTWTRDGGVKTFLDPLFRNGDTSLSIENI 106
Db	588	SSPSLSSSISSTSSASTSSPSISSLSSSISSTSSP 637
QY	107	SQAOAVOCISN-----PSGD--LSSGAGLGPBKENVDEAYT 141
Db	638	SSSIISGSSSISSSISTIPSSSLSTVSSVIPSSTLVSSSL----IVSSSPVA 692
QY	142	GWGRPPQDGPAURATAMIGFGQWLUDGYSATDIWPLVRNDLSVAQYWNQGYDL 201
Db	693	SSSSSPIPSSSSLVST-----YASLNI---THSLSLTM---SSSAI 732
QY	202	WEVGNGSSFFTIAVQHRLALVEGSAFATAVGSS---CWSMCDSQAPELICLVCYLOSWTGFSILA 259
Db	733	PTSVNSNSSLIT-ASSNVNLSSITSSAIVSITVSNISSNLPASATSSQSLTNSSLA 791
QY	260	N-FDSSRSKGDKANTLGSINTDPACADDSTFOCPSPRALANKHKEYVDSRISYTLAND 317
Db	792	TSLYLSSSSSRITSTSSNEYNTSFHAPTWSSTTSSSTTSLLANKGV--NSNITSLN- 848
QY	318	GSDSEAVAVGRYPEPDYNGIPWPLCTLAABEQLYDIALQMDKQGSLEVTDVLDFKA 377
Db	849	-LRESTSSVTSTAVTDSVTS-----TTLTOS-----GRSSSVVSSLSSTS 890
QY	378	L-----YSDAAATGTYSSSSSTYSSIVD-----AVKTFADGFVSVTET 414
Db	891	LSTSIPIPTSSVAPVTSIGSERSSVVGSGTDSATSSWTAETSSAITSVVAASVTPSS 950
QY	415	HAASNGMSEQDKSDBEOLSARDITWSYAAULTTANRNRRNSTVPAWSGETSASSVPG--- 471
Db	951	SSASSNSSSSEVPDSTASATGSS-TSISIATASVSSGSSSTSSVATASANDSSTSSIAASV 1009
Qy	472	TCAATAGTGVSSVTWPSVATGGTTATPTGGSVT-STSKTATASKTSTTRS 530
Db	1010	TGSSTUSVAT-ASVTDSTSSVATASATDSSTSSVATASATDSSTSS 1068
RESULT	15	
Q97BM7	PRELIMINARY;	PRT; 659 AA.
ID	Q97BM7	
AC	097BM7;	
DT	01-OCT-2001 (T-BMBLrel. 18, Created)	
DT	01-OCT-2001 (T-BMBLrel. 18, Last sequence update)	
DE	Glucosamylase.	
GN	Thermaplasmavolcanium.	
OS	Thermaplasmavolcanium.	
OC	Archaea; Buryarchaeota; Thermoplasmatales;	
OC	Thermoplasmataccae; Thermoplasma.	
OX	NCBI_TAXID=50319;	
RN	[1]	
SEQUENCE FROM N A.		
RC	STRAN=GSS1 / DSM 4299 / JCM 9571;	
RX	MEDLINE=20570466; PubMed=1121031;	
RX	Kawasaki T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawamoto T.,	
RA	Kawashima-Ohyba Y., Watanabe K., Yamazaki M., Kaneko K., Kawamoto T.,	
RA	Nunoshiba T., Yamamoto Y., Aranami H., Makino K., Suzuki M.;	
RT	"Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermaplasmavolcanium";	
RT	Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262 (2000).	
RL	EMBL; AP000992; BAB9570.1; -.	
DR	GO; GO:0004339; P:glucan 1,4-alpha-glucosidase activity; IEA.	
DR	GO; GO:0005976; P:polybacccharide metabolism; IEA.	
DR	InterPro; IPR001615; Glyco hydrolase 15.	

Query	Match	Score	DB	Length
Bear	Local Similarity	6.3%;	DB 17;	Length 659;
Matches	90; Conservative	19.7%;	Pred. No. 0.0071;	
	Mismatches	49;	Mismatches	158;
	Indels	159;	Gaps	16;
Qy	57 DSGIVVASPBSTD-----NPDYFTWTRISGLVLUKTLVLDLFRNGDTSLISTIENYISAQAI	111		
Db	304 DLGAIASCDSDILKMSHDDGYYVWPRDASIAAYAL-----SISCHSETARRFFAL	354		
Qy	112 VOGTISNPSPGDLSGGAGLGPKFENDTETATGSM-----GRP-----QDGPPAIRATAMIG	161		
Db	355 MESSMSEEGYLYH-----KVNVD-GKTIASSWLPVHNGKHYPIQSBETAL-----	399		
Qy	162 FGQWILDLNGYSTATDIVPLNR-----NDLSYVAQYMI-----Q	196		
Db	400 -----VVWLWEEFHKKNDIGTRAPYVKEKLITKAADMTRFDSDGIPQ	443		
Qy	197 TGYDWIWEENGGSSFTIAYVORHALVEGSAFATAVGSCSWCDSQABPILCYLOFSWTGSP	256		
Db	444 PSFDLWEEBRYGVHAYTVATAALKAAKSINFANYFGD-----DISEKYLISAERMYEA--	496		
Qy	257 ILLAFDSSRSQKDANTLIGSIHTDPBEAACDDTF---QPCSPRALAHKEVUDSFSI	312		
Db	497 FEBKFYSEEYGYYARIALGKPDPTDVDSALTSIVIFGMKDPRPKIVSTMELI-----	549		
Qy	313 YTLNLDGLSDSEBAVAVGYPEDTYN-----GNPWFCTLAEE--OLYALYWDK	361		
Db	550 --SDTLWINGVGGIARYKONDRTVRVKODTNIONPWNITLMMARRYLRYGPERAWD-	605		
Qy	362 QGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTEADGEVSVIETHAANGS	421		
Db	606 -----LIMWVKSHRQSGI	619		
Qy	422 MSEQYDKSUCQEQSARDLTWSYALLTANRRMSV	457		
Db	620 FSEQQINPYNGQPLSVPLVMSHAIFIISLEYNEBVY	655		

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2004, 17:36:33 ; Search time 18 Seconds
(without alignments)

Run on: June 17, 2004, 17:36:33 ; (without alignments)
1544.748 Million cell updates/sec

Title: US-10-038-723-2

Perfect score: 2771

Sequence: 1 MSFRSLIALSGLVCTGLANV.....SKTTATASAKTSTTRSCMSL 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2742	99.0	640	1 AMYG ASPNG
2	2620.5	94.6	639	1 AMYG ASPNH
3	2588.5	93.4	639	1 AMYG ASPKA
4	1935	69.8	612	1 AMYG ASPOR
5	1577	56.9	626	1 AMYG ARBOR
6	1321	47.7	616	1 AMYG HORRE
7	781.5	28.2	450	1 AMYG SCHPO
8	725	26.2	604	1 AMYG RUOR
9	671.5	24.2	519	1 AMYH SACFI
10	664.5	24.0	519	1 AMYH SACFI
11	641.5	23.2	624	1 AMYH ARXAD
12	597	21.5	549	1 AMYG YEAST
13	522	18.8	767	1 AMYH SACDI
14	521	18.8	768	1 AMYI SACDI
15	221.5	8.0	615	1 YGL0_METJU
16	159.5	5.8	1196	1 ICER_PBSX
17	159	5.7	1210	1 ICEN_PSRPL
18	158	5.7	670	1 YEGG_SCHPO
19	158	5.7	3178	1 YSB9_CABEL
20	157	5.7	1258	1 ICEN_ERWHE
21	156.5	5.6	540	1 GUK1_ASPPAC
22	155.5	5.6	1148	1 ICER_PBSX
23	155	5.6	1322	1 ICEA_PANAN
24	154.5	5.6	1200	1 ICEN_PSESI
25	151.5	5.5	1034	1 ICEN_PANAN
26	151.5	5.5	1306	1 MBB2_YEAST
27	151.5	5.5	1331	1 MANB_CALSA
28	150	5.4	1609	1 FIG2_YEAST
29	150	5.3	507	1 YG46_YEAST
30	142	5.1	1419	1 ALA1_CANAL
31	141.5	5.1	644	1 XND_CELIFI
32	141	5.1	1802	1 HCR1_YEAST
33	140.5	5.1	1567	1 ICEN_XANCT

OC Eukaryota: Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OX Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=A.niger;

RX MEDLINE=8426158; PubMed=6204865;

RA Boel B., Hansen M.T., Hjort I., Hoegh I., Fill N.P.;

RT "Two different types of intervening sequences in the glucoamylase gene from Aspergillus niger.";

RL EMBO J. 3:1581-1585(1984).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=A.niger;

RX MEDLINE=84236105; PubMed=6203744;

RA Boel E., Hjort I., Svensson B., Norris F., Norris K.E., Fill N.P.;

RT Glucoamylases G1 and G2 from Aspergillus niger are synthesized from two different but closely related mRNAs.;"

RL EMBO J. 3:1097-1102(1984).

RN [3]

RP SEQUENCE OF 25-640, AND COMPARISON OF FORMS G1 AND G2.

RC SPECIES=A.niger;

RX MEDLINE=86136085; PubMed=3081341;

RA Svensson B., Larsen K., Gunnarsson A.;"

RT "Characterization of a glucoamylase G2 from Aspergillus niger.";

RL Eur. J. Biochem. 154:497-502(1986).

RN [4]

RP SEQUENCE OF 25-640.

RC SPECIES=A.niger;

RX Svensson B., Larsen K., Svensson I., Boel E.;"

RT "The complete amino acid sequence of the glycoprotein, glucoamylase Gl, from Aspergillus niger.";

RL Carlsberg Res. Commun. 48:529-544(1983).

RN [5]

RP SEQUENCE FROM N.A.

RC SPECIES=A.awamori;

RX MEDLINE=8508534; PubMed=644004;

RA Number J.H., Meade J.H., Cole G., Lawyer F.C., McCabe P.,

RA Schweickart V., Tal R., Wittman V.P., Platgaard J.E., Innis M.A.;

RT "Molecular cloning and characterization of the glucoamylase gene of

Aspergillus awamori.";

RT Mol. Cell. Biol. 4:2306-2315(1984).

RL [6]

RP REVISIONS.

34	138.5	5.0	600	1 SP96 DICDI	P14328 dictyosteli
35	138	5.0	797	1 VGLX HSVEB	P28968 equine herb
36	137	4.9	556	1 WSC3 YEAST	Q12115 saccharomy
37	136	4.9	542	1 CH12 RHOL	P29027 rhizopus ol
38	136	4.9	995	1 YIQ9 YEAST	P40442 saccharomy
39	135.5	4.9	537	1 GU11 PRMJA	Q06886 penicillium
40	133.5	4.8	1589	1 PHP_DROME	P39769 drosophila
41	132	4.8	827	1 XANP XANS2	P06106 xanthomonas
42	130.5	4.7	1537	1 FL01 YEAST	P32768 saccharomy
43	130.5	4.7	1746	1 TENA PIG	Q29116 bus scrofa
44	130	4.7	706	1 PLB2 YEAST	P03674 saccharomy
45	129.5	4.7	1367	1 AMYH YEAST	P08640 saccharomy

ALIGNMENTS

Query Match Similarity 99.0%; Score 2742; DB 1; Length 640;
 Best Local Similarity 99.6%; Pred. No. 9.8e-174; Targets 0;
 Matches 528; Conservative 1; Mismatches 0; Gaps 0;

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>) or send an email to license@isb-sib.ch.
CC
CC
FMRP, DINA60, RAB01254 1...

1	MSPRSLLALSGLVCTGIANVSKRATDSWISNEATYARTAIIANNICGADGAWVGADSGI	60	DR InterPro; IPR00244; CBD_4.
1	MSFRSLALSGLVCTGIANVSKRATDSWISNEATYARTAIIANNICGADGAWVGADSGI	60	DR InterPro; IPR002491; Gluco_glycd_SBD.
61	VVASPTDNPDYFYTWRDGGIVLKTVIIDLFRNGDTSSLSTIENYSAQATVOGINSPPG	120	DR InterPro; IPR00165; Glyco_hydro_15.
61	VVASPTDNPDYFYTWRDGGIVLKTVIIDLFRNGDTSSLSTIENYSAQATVOGINSPPG	120	DR InterPro; IPR00828; Glyco_trane_6hp.
61	VVASPTDNPDYFYTWRDGGIVLKTVIIDLFRNGDTSSLSTIENYSAQATVOGINSPPG	120	DR Pfam; PF0086; Glyco_20_1.
			DR Pfam; PF0086; Glyco_hydro_15_1.
			DR PIRSF; PIRO001031; Gua_Glcsd_SBD; 1.

nucel; IPR000001; **ECOLI**
 InterPro; IPR0020044; CBD_4.
 InterPro; IPR0008291; Glu-a-glycd_SBD.
 InterPro; IPR000165; Glyco_hydro_15.
 InterPro; IPR008928; Glycoco_trans_6hp.
 Pfam; PF00686; CBM_20; 1.
 Pfam; PF00723; Glyco_hydro_15; 1.
 PIRSF; PIRSF00031; Glu-a-glycd_SBD; 1.
 PIRSF; PIRSF00031; Glu-a-glycd_SBD; 1.

OR
PROB: PDB0168; **CBD**: 4; 1.
PS0020: GLUCANOMYLASE; 1.
KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal.

b	301 NHKEVWUDSFRSYLTNLNGLSDSEAVAVGRYPEDTYINGNPWFLCTLAAEQDxDALYQMD	360	FT	194	N-LINKED (GLCNAC: . .)	POTENTIAL.
b	361 KQGSLEVTDVSIDDPFKLYSDAATGTTSSSSSTYSSIVDAVKTFPAGFVSIETHAASNG	420	FT	205	N-LINKED (GLCNAC: . .)	POTENTIAL.
b	361 KQGSLEVTDVSIDDPFKLYSDAATGTTSSSSSTYSSIVDAVKTFPAGFVSIETHAASNG	420	FT	418	N-LINKED (GLCNAC: . .)	POTENTIAL.
b	361 KQGSLEVTDVSIDDPFKLYSDAATGTTSSSSSTYSSIVDAVKTFPAGFVSIETHAASNG	420	SQ	639 AA:	68130 MN:	E93DAE55EEED72326 CRC64;

SEQUENCE	MMW;	E93DAE5BBD72326 CRC64;
CARBONYD	194	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBONYD	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBONYD	418	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	639 AA:	68130 MW;

	Query	Match	93.6%	Score	2620.5;	DB	1;	Length	639;	
	Best Local Similarity	94.3%	Pref. No.	1e-165;						
b	Matches	500;	Conservative	16;	Mismatches	13;	Indels	1;	Gaps	1;
b	QV	1	MSFRSILLASLGLVLTGLANVISKRATLDWSLNSBEATVARTAILNNIGADGAWVGADSGI	60						
b	421	SMSEQYDTSKDSGELSARSDLTVSYAALTANNRRNSVTPASWGETSASAVPGTCATTAIG	480							
b	421	SMSEQYDTSKDSGELSARSDLTVSYAALTANNRRNSVTPASWGETSASAVPGTCATTAIG	480							

Query match 34.0%; Score 2201.5; DB 1; Length 639;
 Best Local Similarity 94.3%; Pred. No. 1e-165; Mismatches 13; Indels 1; Gaps 1;
 Matches 500; Conservative 16; MisMatches 13; Index 1;

	Db
b	1 MSFRSLALUSGLVGLASVISTKRAITDSWLNNEATVARTAILNNIGADGAWNNSGDI 60
481	TYSSVTWPSIVATGGTTATPTGSGSVTAKSTKTTATASKTSTS 530
Qy	61 WASPSTDPRDYFVWTRISGLVLUKLTDLFRNGDTSLSLTINTVISAQAVQGTNSPNG 120

- AMIG ASPSH STANDARD; PRT; 639 AA.
C P22632;
T 01-AUG-1991 (Rel. 19, Created)

121 DLSSGAGLGEGKFNDETAGSMRRQRCGPALRATAMIGFGQMLLDNGYSTATCIVW 180
 121 DLSSGAGLGEGKFNDETAGSMRRQRCGPALRATAMIGFGQMLLDNGYSTATCIVW 180
 121 DLSSGAGLGEGKFNDETAGSMRRQRCGPALRATAMIGFGQMLLDNGYSTATCIVW 180
 121 DLSSG-GLGEIKFNDETAGSMRRQRCGPALRATAMIGFGQMLLDNGYSTATCIVW 179
 121 DLSSG-GLGEIKFNDETAGSMRRQRCGPALRATAMIGFGQMLLDNGYSTATCIVW 179
 121 DLSSG-GLGEIKFNDETAGSMRRQRCGPALRATAMIGFGQMLLDNGYSTATCIVW 179

P
SEQUENCE FROM N.A.
MED-INE=911B2400; PubMed=1368603;

300 NEKEDSERSTYTT NDGT SDSEA VAGRDENS YNGNDBET CTL MAAFO YDAI YWOD 359

RESULTS ...
"Molecular cloning of the Glucosidase gene of *Aspergillus shirousami* and its expression in *Aspergillus oryzae*."
Agric. Biol. Chem. 54:1905-1914(1990).

-1- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose

361 KQGSLEVTDVSLDFKALYDAATGTYSSSTVSI VDAVKTFADGFVSVTHAASNG 420
 360 KQGSLEBTDVSLDFKALYSGAATGTYSSSTVSI VSAVTFADGFVSVTHAASNG 419
 421 SMSEBDXKSPQEQSLARDLWMSYALLTANRNRNVPASWGETSASAVSGTCATAIG 480

Simularia belongs to family 13 of glycosyl hydrolases.

SUSSEDFURSKUGELLSARLUNINSINALLIANRKNVFFSMUEISASSVFGICMAISAGG 473

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Please see and for commercial

RA Hoheisel J.D., Fartmann B., Nakamura G., Kempken F., Maier J.,
 RA Schulte U.; "What's in the genome of a filamentous fungus? Analysis of the
 RT genome sequence." *Neurospora* 31:1944-1954 (2003).
 RL Nucleic Acids Res. [3]

RP SEQUENCE OF 36-65.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RA Koh-Luar S.I., Parish J.H., Bleasby A.J., Pappin D.J.C., Ainley K.,
 RA Johansen P.E., Radford A.; "Exported proteins of *Neurospora crassa*: 1-glucosamylase.",
 RL Enzyme Microb. Technol. 11:692-695 (1999).
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
 glucose residues successively from non-reducing ends of the chains
 with release of beta-D-glucose.

CC -!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial/
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC

DR EMBL; X67291; CAA47071; -.
 DR IEMBL; AL335932; CAB914261; -.
 DR HSSEB; P04464; 1GAT.
 DR InterPro; IPR00204; CBD_4.
 DR InterPro; IPR008291; Glu-a-glcid_SBD.
 DR InterPro; IPR00165; Glyco_hydro_15.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00685; CBM_20_1.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR PRINTS; PIR0736; Glu-a-glcid_SBD; 1.
 DR PRODOM; PDO01568; CBD_4; 1.
 DR PROSITE; PS00820; GLUCAMYLASE; 1.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; glycoprotein;
 KW Signal.
 FT PROPEP 1 19 POTENTIAL.
 FT PROPEP 20 35 POTENTIAL.
 FT CHAIN 36 626 GLUCAMYLASE.
 FT BINDING 155 155 SUBSTRATE BY SIMILARITY.
 FT ACT_SITE 211 211 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 214 214 GENERAL ACID CATALYST (BY SIMILARITY).
 FT ACT_SITE 215 215 INTERACT WITH SUBSTRATE (BY SIMILARITY).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) POTENTIAL.
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 82 82 MISSING '(IN REF. 1).
 FT CONFLICT 550 550 A -> R (IN REF. 1).
 FT CONFLICT 560 560 V -> L (IN REF. 1).
 FT SEQUENCE 626 AA; 664 AA; 5AE5BDDBA7A38349 CRC64;

Query Match 56.9%; Score 1577; DB 1; Length 626;
 Best local Similarity 57.6%; Pred. No. 8.6e-97; Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;

Qy 2 SFRSLALSGLCLVGLANVISKRATLDMSNEATVAPALINNIGADGAWSGADSGIV 61
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 13 AFOAVTGLDPPLHEKRHSIDIKR-SVDSYQTETPIAKNLCHMGASCGRAGSAASGVW 71
 Db 62 VASPTSDNPDYFYTWRDSDLVLUKTKLVDLDTSLISTENIYSAQIVQGTSNPG 120
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 72 VASPSKSSPDWYTWTRDAALVTKLVDLDTNDTNTQIAYAAQMLQGVSNPG 131
 SQ

RESULT 6 AMYG_HORRE STANDARD; PRT; 616 AA.
 ID AMYG_HORRE
 AC Q03045;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Glucoamylase P precursor (EC 3.2.1.3.) (Glucan 1,4-alpha-glucosidase)
 GN GAMP.
 OS Hormoconis resinae (Cerebella fungus) (Amorphotheca resinae).
 OC Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
 OC Amorphothecaceae; Amorphotheca.
 OX NCBI_TAXID=5101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 20495;
 RA Joutsjoki V.V., Torkkeli T.K.;
 RT "Glucoamylase P gene of Hormoconis resinae: molecular cloning,
 sequencing and introduction into *Trichoderma reesei*.",
 RL FEBS Microbiol. Lett. 78:237-243(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 20495;
 RX MEDLINE:93365035; PubMed:8358830;
 RA Vainio A.E.I., Torkkeli H.T., Tuusa T., Aho S.A., Fagerstroem B.R.,
 RA Korhola M.P.; "Cloning and expression of Hormoconis resinae glucoamylase P cDNA in
 Saccharomyces cerevisiae.",
 RT Curr. Genet. 24:38-44(1993).
 RL CURR GENET [3]
 RP SEQUENCE OF 72-75, AND CHARACTERIZATION.
 RX MEDLINE:90318987; PubMed:2116499;
 RA Fagerstroem R., Vainio A.E.I., Suoranta K., Pakula T., Kalkkinen N.,
 RT "Comparison of two glucosamylases from Hormoconis resinae.",
 RL J. Gen. Microbiol. 136:913-920(1990).
 -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucos residues successively from non-reducing ends of the chains
 with release of beta-D-glucose.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial/
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

Db 192 PIVRNNDLVATAQYNNNTCDLWEEVNSSFFTAASHHALVGSAPAKSVGSSCSACDAI 251
 QY 241 APEIICLYQSFWTGCS-FILANFDSSRSQKDANTLIGSHTFDEAACDSTFOPCSPDL 299
 Db 252 APQLCFQSFWSNGVYISNFVNRSKDINSVLTSIHFDPAGCVNTQPCSDAI 311
 QY 300 ANHKEVWVPSRSTYTLNGQLSDBAVAFGRYEPDFTYGNPWFCTLAQAEQYDALQW 359
 Db 312 ANHKVWVDSMR-FMWGVNSRTAGKAAAGRGADEVYNGNPWFLAHLAEQDLYAVW 370
 QY 360 DKQCSLEYTDVSDPPKLYSDATGTVSSSSSTSYSSVDAVKUTFADGFVSTVETHASN 419
 Db 371 KKQOSITVNTSLAFLPKOLVPSVSTGTYSSSSSTVTAI NAVITYADGFVDIVAQYTESD 430
 QY 420 GSMSBQYQKSDGEOLSARDLTMWSYALLTANNRNSVPSKGTSASSVPGTCAMSAI 479
 Db 431 GSLEAQFKDQSGAPLSAHLTMWSYASESAARRAGTIPPSIGCAASANSLPGCSASTVA 490
 QY 480 GTSSSVTNTSWPSVIVATCCTTTR-ATPFGSGS----VTSKTKTATSKT 524
 Db 491 GSTATATATSFPAINTPASTTVPPQTQTCACADEHVLYTFNEKVTSYGQT 541

CC or send an email to license@ibb-sib.ch.

DR EMBL: X68143; CAA48243.1; -
DR EMBL: X67708; CAA47945.1; -
DR PIR: S33908; S33908.
DR HSSP: P04664; IGA1.
DR InterPro: IPR020244; CBD_4.
DR InterPro: IPR008291; Glu-a-glycol_SBD.
DR InterPro: IPR000165; Glyco_hydro_15.
DR InterPro: IPR008928; Glyco_trans_6hp.
DR Pfam: PF00686; CBM_20; 1.
DR Pfam: PF00723; GLYCO_hydro_15; 1.
DR Pfam: PF00800; Glu-a-glycol_SBD; 1.
DR Prints; PRO0736; GLYDRMLSB15.
DR Prod0m: PRO0156; CBD_4; 1.
DR Prosite; PS00820; GLUCOAMYLASE; FALSE_NEG.
DR KW Hydrolase; Glycosidase; Polysaccharide_degradation; Glycoprotein;
Signal; 1
KW SIGNAL; 1
FT CHAIN 30
FT BINDING 149
FT ACT_SITE 205
FT ACT_SITE 208
FT ACT_SITE 209
FT CARBOHYD 200
FT CARBOHYD 427
SQ SEQUENCE 616 AA; 66432 MW; -B5F4DC8EBBB152FB CRC64;

Query Match Score 47.7%; Score 1321; DB 1; length 616;
Best_Local_Similarity 48.6%; Pred 6.8e-80; Mismatches 150; Indels 34; Gaps 6;
Matches 257; Conservative 88; MisMatches 150; Indels 34; Gaps 6;

[1] SEQUENCE FROM N.A.

STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hanlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitzsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volkzaert G., Aert R., Robishaw J., Grymonprez B.,
Weltien I., Vansteelandt E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedder H., Wambutt R., Purnelle B.,
Gorfeau A., Cadieu E., Dreano S., Gloux S., Leilaure V., Mottier S.,
Galibert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gallardot C., Tallada V., Garzon A., Thode G.,
Daga R.R., Cruado L., Jimenez J., Sanchez M., del Rey F., Benito J.J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Ra Cerruti L., Lowe T., McCormick W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Usbiry D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.,"
RA Nature 415:871-880(2002).
RN [2]

RP SEQUENCE OF 210-450 FROM N.A.

RC STRAIN=CD16-1;

RX MEDLINE=21270454; PubMed=11376151;

RX Watanabe T., Miyashita K., Saito T.T., Yoneki T., Kakihara Y.,
RA Nabetoh K., Ishii Y.A., Shimoda C., Nojima H.,
"Comprehensive isolation of meiosis-specific genes identifies novel
proteins and unusual non-coding transcripts in Schizosaccharomyces
pombe";
RT Nucleic Acids Res. 29:2327-2337(2001).

CC

DR PRINTS; PR00736; GLYHYDRASE5.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
 KW Signal; Meiosis.
 FT SIGNAL 1 16 POTENTIAL.
 PROPEP 17 28 BY SIMILARITY.
 FT CHAIN 29 450 PROBABLE GLUCOAMYLASE.
 FT BINDING 147 147 SUBSTRATE (BY SIMILARITY).
 FT ACT_SITE 203 203 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 206 206 GENERAL ACID CATALYST (BY SIMILARITY).
 FT ACT_SITE 207 207 INTERACT WITH SUBSTRATES (BY SIMILARITY).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC . .) (POTENTIAL).
 SEQUENCE 450 AA; 51163 MW; 31C5BF2ABE4785FE CRC64;

Query Match 28.2%; Score 781.5; DB 1; Length 450;
 Best Local Similarity 37.6%; Pred. No. 1.9e-44; Matches 179; Conservative 68; Mismatches 166; Indels 63; Gaps 12;

QY 7 DASGLIVCTG--LAVNIRSLWSNEATARTAQNIGADGAWSGADSGIWA 63
 8 LLLGGVNSAABSLSPNPKRSKESADMEDWTPOKGIGMNGMNGSMGEAKDINGPCIA 67

QY 64 SPSTNDPFDYTWDRDSGIVLTAKTVDLFENGDTSLSTENIYSAQATVQGISPGDLS 123
 68 SPSTDSPDYYQWDRDSLTTMTLDRFBDGKSLPEPLIVYKMDMVRQLQKVNPNSDFY 127

QY 124 SAGLGKEPKENDDTAYTGSWGRQFDGQALLRATAMIGQFCQWLDNGYSTATDIVPLV 183
 128 AG-SLGERPKENPDTSYDSDWGRFONDSPALARATAFIKYNNLFFENGKEVHEVWIAV 186

QY 184 RNDLSYVAQWQNQGYDLMVEBVNGSSFFTAVQVRAVLVEGSAFAVASSCSWCDSQAE 243
 187 LADDDYTANHWEATSFDLREBEEKWHIFTLAVQGRAMQDGTAFAKRIG-----APD 237

QY 244 -ILCYLQSFW-TGSFILAFDS-S-SRGIDANTLGSHT-FDPEAACD 287
 238 QALIVQRTIEPDQKJGFEPWDPGMVGVIKGRVDRSGIJCSTIASLYSNEFD----- 291

Db HSP; P04064; 1GAT.

QY 288 DSTROPCSPRALAHKKEVUDPSRSIYTLLDGLSSEAVAVGRYPTDTN---GNMP 342
 292 -MHLILPTLUKQBTMTRDYPVNQGWQ---AMGRYPEPDVTDGVSKSIGNPWF 339

Db DR InterPro; IPR000165; Glyco_trans_15.

QY 343 LCTLAAREQDIAJQWQDKQSLVTDVSDLDFK-ALISDAATGTYSSSSTSIIVA 400
 340 ICITSSAAETIYKAIAYDVNGKLPPELTENVHFFMKFAERGD-----PYINNSVIRKN 390

Db DR PRINTS; PR00736; GLYHYDRASE5.
 PROSITE; PS00820; GLUCOAMYLASE; 1.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
 KW Signal. 1 25

FT SIGNAL 1 25
 FT CHAIN 26 604 GLUCOAMYLASE 1 (GLUC 1).
 FT DOMAIN 116 604 GLUCOAMYLASE 2 (GLUC 2).
 FT DOMAIN 26 109 GLUCOAMYLASE 3 (GLUC 3) (OR 110-604).
 FT BINDING 116 604 STARCH DEGRADATION (OR 110-604).

FT ACT_SITE 336 336 SUBSTRATE (BY SIMILARITY).
 FT ACT_SITE 339 339 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 340 340 GENERAL ACID CATALYST (BY SIMILARITY).
 SEQUENCE 604 AA; 65162 MW; 78421F1AA93ADBS4; CRC64;

Query Match 26.2%; Score 725; DB 1; Length 604;
 Best Local Similarity 36.8%; Pred. No. 1.6e-40; Matches 165; Conservative 71; Mismatches 170; Indels 42; Gaps 10;

RESULT 8
 AMYG_RHTOR STANDARD; PRT; 604 AA.

AC P07683; DT 01-APR-1988 (Rel. 07, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-Mar-2000 (Rel. 39, Last annotation update)
 DE Glucoamylase precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
 DE (1,4-alpha-D-glucan glucohydrolase).
 OS Rhizopus oryzae (Rhizopus delimita).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Rhizopus.
 RN [1] NCBI_TaxID=64495;
 RP SEQUENCE FROM N.A.

RC STRAINSAM0034;
 RA Asikari T., Nakamura N., Tanaka Y., Kiuchi N., Shibano Y.,
 RA Tanaka T., Amachi T., Yoshiyumi H.,
 RT "Rhizopus" raff-starch-degrading glucoamylase: its cloning and
 RT expression in yeast.;
 RL Agric. Biol. Chem. 50:957-954 (1986).

QY 25 ATUDSWLWSNEATARTAQNIGADGAWSGADSGIWAASPSTNDPFDYTWDRDSQIVL 84
 Db 168 STISSWIKKQEGJSRFAMLRNINP---PGSATGPFIASLSPAGPDQYAWRDALTS 222
 QY 85 KTLVLDFLR---NGDTSLSTENIYSAQATVQGISPNRGDLSGGAGLGPBKPKENDEAYT 141
 Db 223 NVTVYEYNTLGSNKTILVNLKQYTFVKVSTSTVCN-----CLGPKPKNDASGYT 276

QY 142 GSQGRPQDPGPAARATAMIGFG-QMLLDNGYSTATDIVPLVYRNDLSSYQAQWNQTYD 200
 277 GAMGRPQDGAERATTFILAFDSLTYQTKDASVYTGTPKAIFKDLIYVUNWSNGCFD 336

Db 337 LWEEVNGSFFTAVQHDLVEGSAFAVAGSS--CSVCDSOAPEILCYLQSTWTGSPIL 258

QY 201 LWEEVNGSFFTAVQHDLVEGSAFAVAGSS--CSVCDSOAPEILCYLQSTWTGSPIL 258

Db 337 LWEEVNGSFFTAVQHDLVEGSAFAVAGSS--CSVCDSOAPEILCYLQSTWTGSPIL 258

QY 259 ANFDS---SRSGKDNT---LGSIHTFDPPEACDDSTROPCSPRALAHKKEVDS 308
 Db 397 IOVSOSVTGGVSKGLDVTLLANLGSV-----DDGFTPGSKLATAVAVEDS 447

QY 309 FRSIYTLLDGLSSEAVAVGRYPTY---YNGNPFLCTLAACQDLYQWQKG 363

Db 448 FASLYPINKNLUISYLVGNISGRYPEDTYNGNNSQGNSWFLAVTGVALYVRAKEWIGNG 507
Qy 364 SLEVTQVSLPDKKALPSDAAG-TYSSSSYVSYTIDAVKTFADGVSVIETHAASNGM 422
Db 508 GIVYVSSISLPPFKPDSATGCKYKVGTSPFNNLAQNTIAADRFLSTVOLHARINGSL 567
Qy 423 SEQYDVKSDGEQLSARDITWSYAAHLTAN 450
Db 568 AEEFDRTGJGUSGARDITWSYAAHLTAN 595

RESULT 9

AMYH_SACFI STANDARD; PRT; 519 AA.

ID AMYH_SACFI STANDARD; PRT; 519 AA.

AC P26289; P28745; 01-AUG-1992 (Rel. 23, Created)
DT 15-JUL-1998 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 38, Last annotation update)

DB Glucoamylase GLU1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucosidase) (1,4-alpha-D-glucan glucohydrolase). GLA1.

OS Saccharomyces fuliginea (Yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycopsidae; Saccharomyces; OX NCBI_TaxID=4944; RN [1]
RC STRAIN=KZ;
RX MEDLINE=91137640; PubMed=1840332;
RA Hostanova E., Balanov J., Gasperik J.; RT "The nucleotide sequence of the glucoamylase gene GLU1 from Saccharomyces fuliginea KZ.";
RL FEMS Microbiol. Lett. 67:103-108(1991). RN [2]
RP REVISIONS.
RC STRAIN=KZ;
RA Hostanova E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.

CC -!- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES. ONLY DIFFERS IN 11 POSITIONS WITH GLUCOAMYLASE GLU1.

RESULT 10

AMYH_SACFI STANDARD; PRT; 519 AA.

ID AMYH_SACFI STANDARD; PRT; 519 AA.

AC P08017; 01-AUG-1998 (Rel. 08, Created)
DT 15-AUG-1998 (Rel. 08, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Glucoamylase GLU1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucosidase) (1,4-alpha-D-glucan glucohydrolase). GLU1.

OS Saccharomyces fuliginea (Yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; OX NCBI_TaxID=4944; RN [1]
RP REVISIONS.
RA Itoh T., Ohtsuki I., Yamashita T., Fukui S.; RT "Nucleotide sequence of the glucoamylase gene GLU1 in the yeast Saccharomyces fuliginea". J. Bacteriol. 169:4171-4176(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=8730799; PubMed=3114236;
RA Sevcik J., Solovicova A., Hostanova E., Gasperik J., Wilson K.S., Dauter Z.; RT "Structure of glucoamylase from Saccharomyces fuliginea at 1.7-A resolution.". RRL Acta Crystallogr. D 54:854-866(1998); CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.

CC -!- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES. ONLY

Best Local Similarity 35.2%; Pred. No. 4.3e-37;
Matches 173; Conservative 73; Mismatches 169; Index 77; Gaps 16;

Db 139 TAVTGKWRQRDGPRALATM-----IGFCOMW---DNGYTTSTDIDWPLVR 184
Db 160 SAYTGAWGRPGNDGPALARAVISYRVDVNLNSLINKSKVLTUDSGDNFSST-EDIVNNIK 218
Qy 185 NDLSYYAQYWMQTGYDMLWEENVGSSFTTIAVORHALV-----EGSATATAVGS 235
Db 219 PDLEVIGWYSTGWSTGEMLWENGRHTTSVQKALAYVADIASKEDGFTANTISSTAS 278
Qy 236 WCDSDAREFELLCYQLQSFWTGS-----FILANPD---SSRSCKDANTLIGSHTFD 281
Db 279 -----TLESYLSGSDGGFVNIDVNHVENDPDLQNSRGQIDSATVIGPLTHD 327
Qy 282 PRACACDSDTFRCPSPALANKHEVUDVSRSYTLANGLSSEAVANGRYBEDY---Y 336
Db 328 -IGESESTPFDVNEVTLQSYLBDNKORYSVNSAY-SAGAAGRYPEDVYNGDSS 384
Qy 337 NGNPWFLCTLAAEQLDQYDQKOGKSEVT-DVSLDFKALVSDAAT----- 384
Db 385 EONPWLATVAYAQVWKLVD-ANSSANDTINKNIDFNKYYVUDSTINSQSSD 443
Qy 385 GTYSSSSYTSSIVDVKTFADGFVISVETHAASNGMSMSQYDKSDGEQLSARDITWSY 444
Db 444 VTIKSGSDEFNTVADNLVFGDSFLQVILDHINDGSLNEBOLNRVYGSISAYSILTWSG 503
Qy 445 ALTTAIIIRRNRSV 456
Db 504 ALLEAIRLRNRY 515

CC DIFFERS IN 11 POSITIONS WITH GLUCOAMYLASE GLA1.

DIFFERS IN 11 POSITIONS WITH GLUCOAMYLASE GLA1.

FT HELIX 303

309

FT	HELIX	303	307
FT	TURN	308	309
FT	TURN	316	316
FT	HELIX	317	325
FT	TURN	328	329
FT	TURN	338	339
FT	HELIX	341	357
FT	HELIX	359	363
FT	TURN	374	375
FT	STRAND	378	378
FT	STRAND	383	383
FT	STRAND	389	389
FT	HELIX	390	410
FT	TURN	411	411
FT	STRAND	414	417
FT	HELIX	418	420
FT	HELIX	421	427
FT	TURN	428	428
FT	HELIX	431	433
FT	TURN	434	434
FT	TURN	436	437
FT	HELIX	438	440
FT	STRAND	443	446
FT	TURN	448	449
FT	HELIX	451	474
FT	TURN	477	478
FT	STRAND	484	485
FT	TURN	487	489
FT	STRAND	492	493
FT	TURN	496	497
FT	HELIX	499	519
SQ	SEQUENCE	519 AA;	57539 MN;
			BB73035AD1B77652 CRC64;

RESULT 11	
AMYG_ARXAD	STANDARD; PRT; 624 AA.
AC P42042;	
DT 01-NOV-1995 (Rel. 32; Last sequence update)	
DT 10-OCT-2003 (Rel. 42; Last annotation update)	
DE Glucosidase precursor (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucan glucohydrolase)	
GN GAA.	
OS <i>Axula adenivorens</i> (Yeast)	
OC Saccharomyctetes; Dipodascaceae; mitosporic Dipodascaceae; <i>Axula</i> .	
OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
OC NCBI_TaxID:37620;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Manteuffel R., Kunze G.;	
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ database.	
CC - CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains	
CC with release of beta-D-glucose.	
CC - SIMILARITY: Belongs to family 15 of glycosyl hydrolases.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RESULT 12	
AMYG YEAST	STANDARD; PRT; 549 AA.
AC P0019;	
DT 01-AUG-1988 (Rel. 08; Created)	
DT 01-FEB-1995 (Rel. 31; Last sequence update)	
DT 10-OCT-2003 (Rel. 42; Last annotation update)	
DE Glucosidase, intracellular sporulation-specific (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucan glucohydrolase).	
GN SGA1 OR SGA OR YIL099W.	
OS Saccharomyces cerevisiae (Baker's Yeast).	
OC Saccharomyctetes; <i>Saccharomyces cerevisiae</i> (Baker's Yeast);	
OC HSSP; P04694; IGA1.	
DR InterPro; IPR00116; Glyco_hydro_15.	
DR InterPro; IPR005928; Glyco_trans_6mp.	
DR Pfam; PF00723; Glyco_hydro_15; 1.	
DR PRINS; PR0736; GLYHDRASB15.	
DR PROSITE; PS0820; GLUCOAMYLASE; 1.	
KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal.	
KW SIGNAL 1 18 POTENTIAL.	
FT CHAIN 19 624 GLUCOMYLASE.	
FT ACT SITE 340 340 CATALYTIC BASE (BY SIMILARITY).	
FT ACT SITE 343 343 GENERAL ACID CATALYST (BY SIMILARITY).	
FT ACT SITE 344 344 INTERACT WITH SUBSTRATES (BY SIMILARITY).	
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO SEQUENCE 624 AA; 68980 MW; 74C0CDFB43FF71B4 CRC64;	
Query Match 23.2%; Score 641.5; DB 1; Length 624;	
Best Local Similarity 32.8%; Pred. No. 5.3e-55; Gaps 13;	
Matches 154; Conservative 90; Mismatches 172; Indels 53; Gaps 13;	
OY 27 LDSLW!-SNEAT--VARTAILNIGAGAWM!GAGSGADG!GIVWASPSTNPDVYTW!TWSLGL 82	
OY 160 ITW!W!KPSNSDQGIAKSFLRNN!----!P!GAPE!VIAQSYSPBDYATW!WDASL 214	
OY 83 V!KLT!W!LFRNGDTS!LISTIEN!VISAQIVOGCISNSPGDLSGAG!CEPKWT!VDEAYTG 142	
OY 215 VMDVWVRLYSSAKSEERKOLYVEKIL!FOYAKG-AQ!OND!P!AISG!GEPEK!V!NTAFTG 273	
CC - SIMILARITY: Belongs to family 15 of glycosyl hydrolases.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RESULT 13	
AMYG YEAST	STANDARD; PRT; 549 AA.
AC P0019;	
DT 01-AUG-1988 (Rel. 08; Created)	
DT 01-FEB-1995 (Rel. 31; Last sequence update)	
DT 10-OCT-2003 (Rel. 42; Last annotation update)	
DE Glucosidase, intracellular sporulation-specific (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucan glucohydrolase).	
GN SGA1 OR SGA OR YIL099W.	
OS Saccharomyces cerevisiae (Baker's Yeast).	
OC Saccharomyctetes; <i>Saccharomyces cerevisiae</i> (Baker's Yeast);	
OC HSSP; P04694; IGA1.	
DR InterPro; IPR00116; Glyco_hydro_15.	
DR InterPro; IPR005928; Glyco_trans_6mp.	
DR Pfam; PF00723; Glyco_hydro_15; 1.	
DR PRINS; PR0736; GLYHDRASB15.	
DR PROSITE; PS0820; GLUCOAMYLASE; 1.	
KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal.	
KW SIGNAL 1 18 POTENTIAL.	
FT CHAIN 19 624 GLUCOMYLASE.	
FT ACT SITE 340 340 CATALYTIC BASE (BY SIMILARITY).	
FT ACT SITE 343 343 GENERAL ACID CATALYST (BY SIMILARITY).	
FT ACT SITE 344 344 INTERACT WITH SUBSTRATES (BY SIMILARITY).	
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO SEQUENCE 624 AA; 68980 MW; 74C0CDFB43FF71B4 CRC64;	
Query Match 23.2%; Score 641.5; DB 1; Length 624;	
Best Local Similarity 32.8%; Pred. No. 5.3e-55; Gaps 13;	
Matches 154; Conservative 90; Mismatches 172; Indels 53; Gaps 13;	
OY 27 LDSLW!-SNEAT--VARTAILNIGAGAWM!GAGSGADG!GIVWASPSTNPDVYTW!TWSLGL 82	
OY 160 ITW!W!KPSNSDQGIAKSFLRNN!----!P!GAPE!VIAQSYSPBDYATW!WDASL 214	
OY 83 V!KLT!W!LFRNGDTS!LISTIEN!VISAQIVOGCISNSPGDLSGAG!CEPKWT!VDEAYTG 142	
OY 215 VMDVWVRLYSSAKSEERKOLYVEKIL!FOYAKG-AQ!OND!P!AISG!GEPEK!V!NTAFTG 273	
CC - SIMILARITY: Belongs to family 15 of glycosyl hydrolases.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RESULT 14	
AMYG YEAST	STANDARD; PRT; 549 AA.
AC P0019;	
DT 01-AUG-1988 (Rel. 08; Created)	
DT 01-FEB-1995 (Rel. 31; Last sequence update)	
DT 10-OCT-2003 (Rel. 42; Last annotation update)	
DE Glucosidase, intracellular sporulation-specific (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucan glucohydrolase).	
GN SGA1 OR SGA OR YIL099W.	
OS Saccharomyces cerevisiae (Baker's Yeast).	
OC Saccharomyctetes; <i>Saccharomyces cerevisiae</i> (Baker's Yeast);	
OC HSSP; P04694; IGA1.	
DR InterPro; IPR00116; Glyco_hydro_15.	
DR InterPro; IPR005928; Glyco_trans_6mp.	
DR Pfam; PF00723; Glyco_hydro_15; 1.	
DR PRINS; PR0736; GLYHDRASB15.	
DR PROSITE; PS0820; GLUCOAMYLASE; 1.	
KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal.	
KW SIGNAL 1 18 POTENTIAL.	
FT CHAIN 19 624 GLUCOMYLASE.	
FT ACT SITE 340 340 CATALYTIC BASE (BY SIMILARITY).	
FT ACT SITE 343 343 GENERAL ACID CATALYST (BY SIMILARITY).	
FT ACT SITE 344 344 INTERACT WITH SUBSTRATES (BY SIMILARITY).	
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO SEQUENCE 624 AA; 68980 MW; 74C0CDFB43FF71B4 CRC64;	
Query Match 23.2%; Score 641.5; DB 1; Length 624;	
Best Local Similarity 32.8%; Pred. No. 5.3e-55; Gaps 13;	
Matches 154; Conservative 90; Mismatches 172; Indels 53; Gaps 13;	
OY 27 LDSLW!-SNEAT--VARTAILNIGAGAWM!GAGSGADG!GIVWASPSTNPDVYTW!TWSLGL 82	
OY 160 ITW!W!KPSNSDQGIAKSFLRNN!----!P!GAPE!VIAQSYSPBDYATW!WDASL 214	
OY 83 V!KLT!W!LFRNGDTS!LISTIEN!VISAQIVOGCISNSPGDLSGAG!CEPKWT!VDEAYTG 142	
OY 215 VMDVWVRLYSSAKSEERKOLYVEKIL!FOYAKG-AQ!OND!P!AISG!GEPEK!V!NTAFTG 273	
CC - SIMILARITY: Belongs to family 15 of glycosyl hydrolases.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

DR HSSP; P08017; IAYX.
 DR Germonline; 139634; -.
 DR SGD; SGD1361; SGAI.
 GO; GO-0001024; C-vacuole (sensu Fungi); IDA.
 GO; GO-0004339; F-Glucan 1,4-alpha-glucosidase activity; IDA.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008228; Glyco_trans_6hp.
 DR PRINTS; PRO0736; GLHYDYLASE15.
 DR PROSITE; PS00820; GLUCOAMYLASE_1.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; Sporulation.
 FT BINDING 198 198 SUBSTRATE (BY SIMILARITY).
 FT ACT_SITE 261 261 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 264 264 GENERAL ACID CATALYST (BY SIMILARITY).
 FT ACT_SITE 265 265 INTERACT WITH SUBSTRATES (BY SIMILARITY).
 FT CONFLICT 504 549 HVGTDGELSEQQNKVTKFGMGAQHLYTWSYTSFWDAYQIRQE
 VLGDL -> TWEQPGN (IN REF. 1).
 SQ SEQUENCE 549 AA; 61463 MW; 6351E94F2CF4AB77 CRC64;
 Query Match Best Local Similarity 30.4%; Pred. No. 3.9e-32; Matches 153; Conservative 89; Mismatches 202; Indels 60; Gaps 14; Gapopen 14;
 Qy 1 MSFRRSLLASGLGVLCTGLANWISKERATDLSWLNATVARTAUNNIGADAWWGSAGSGI 60
 Db 56 VQLRDAVLMNGTVVYD-SNGAWNSALBEWMLQGOKKVSLKIFENIGPSAVYPS-ISPGV 113
 Qy 61 VVASPSTNDPDPFYTWTRSGVLUKLVLDFRNGDTSLISTENVISQAOIVQGINSQ 120
 Db 114 VIASPSQTHPDYFYQWIRDSLALTINSIVS--HSAGPAETLQYLVNSFHLGRSN-- 167
 Qy 121 DLSSGAG----LGEPEPKENVDETAVGWSWRGRDGFALLRATAAMIGFQWILDNG-- 170
 Db 168 TLGAGIGYVNTDVAGDPKRNVDNATAFDWGRFQNDGEARSIAIKIKIDYIKQSGDL 227
 Qy 171 ----YTSPTADYIPLVRLNDLSTVAQYMNQTGIDLWEVNGGSSPFTAVORHALVESEA 225
 Db 228 GAKYKPFOSTA-DIFDDIVRMLRFLIDHMNSGFDLWEBVNMGHFFTLVQLSAVDKSIS 286
 Qy 229 FATAVGSSCSWMD---SQREPEILCYL---QSFVWGSFLIANF-----DSRSRGKA 270
 Db 287 YFNASERSSPPVEBLROTDRDISKFLVDPANGFINGKY--NYIVGTPMIA/DTDLRSGLDI 343
 Qy 271 NTLIGSIHTFPDEACDSTFPQCPSPRALJAHKEVWDVSDRSIYTFLNDGLSSEAVGRY 330
 Db 344 STLLAANTVHDAPSA-SHIPPFINDPAVANTLHILMLHRSIVKINDSSKKATGIALGRY 402
 Qy 331 PEDTY----YNGPWFCLTAAABOLPOLYQYDQKQSLEVDTVSLOPKALYSDAATG 385
 Db 403 PEDVYDGIGFGEGNPWLATCTASTLYQYLRHISEQHDLLVVMNIDSNAFWSELVFS 462
 Qy 386 TYSS-----SSSTYSSVDAVKTFPQDFPVSLIVETHAASNMSMSEQVQDSBEGQ 433
 Db 463 NLTFLGLNDGEGYLILEFTPAFQHPIOKIFQALADSFLVLUKAVHGTDGELSEQQNKYTFM 522
 Qy 434 LSARDLTWSYALLTANNERNSW 457
 Db 523 QGAQHLTWSYTFMDAYQIROEVL 546
 RESULT 13
 AMY_SACDI STANDARD PRT; 767 AA.
 ID AMYH_SACDI STANDARD PRT; 767 AA.
 AC P04065; Q92314; DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Glucosaminidase SI precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
 DB (1,4-alpha-D-glucan glucohydrolase) (GAL).
 OS Saccharomyces diatacticus (yeast).
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 SQ SEQUENCE 767 AA; 82488 MW; A5F29B2427EDB593 CRC64;
 Query Match Best Local Similarity 30.5%; Pred. No. 5.9e-27; Matches 139; Conservative 80; Mismatches 177; Indels 60; Gaps 15;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OK NBI_TAXID=11870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 60705;
 RX MEDLINE=85104778; PubMed=3918017;
 RA Yamashita I., Suzuki K., Fukui S.;
 RT "Nucleotide Sequence of the extracellular glucoamylase gene STA1 in
 the Yeast *Saccharomyces diastaticus*."
 RL J. Bacteriol. 161:567-573(1985).
 RN [2]
 RP SEQUENCE OF 1-54 FROM N.A.
 RA Yamashita I., Suzuki K., Sakuzo F.;
 RT "Proteolytic processing of glucoamylase in the yeast *Saccharomyces cerevisiae*."
 RL Agric. Biol. Chem. 53:749-755(1989).
 CC [3]
 CC SEQUENCE OF 1-54 FROM N.A.
 RA Shima H., Inui M., Akeda R., Yamashita I.;
 RT "Upstream regions of the yeast glucoamylase gene which are required for efficient transcription.";
 RL Agric. Biol. Chem. 53:749-755(1989).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucosidic residues successively from non-reducing ends of the chains with release of beta-D-glucose.
 CC -!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X02649; CAL26487.1; ALT_INIT.
 DR EMBL; D00428; BAD00332.1; -.
 DR PIR; A12186; ALBYC.
 DR HSSP; P08017; IAYX.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008228; Glyco_trans_6hp.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR PROSITE; PS00820; GLUCOAMYLASE_1.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 767 GLUCOAMYLASE_1.
 FT DOMAIN 22 347 SER/THR/RICH.
 FT DOMAIN 348 691 H SUBUNIT.
 FT DOMAIN 692 767 Y SUBUNIT.
 FT BINDING 455 455 SUBSTRATE (BY SIMILARITY).
 FT ACT_SITE 518 518 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 521 521 GENERAL ACID CATALYST (BY SIMILARITY).
 FT ACT_SITE 522 522 INTERACT WITH SUBSTRATES (BY SIMILARITY).
 FT CARBOHYD 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 546 546 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 650 650 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 720 720 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 741 741 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 767 AA; 82488 MW; A5F29B2427EDB593 CRC64;

RESULT 15
 YG10 MENJA STANDARD; PRT; 615 AA.
 ID -YG10 MENJA STANDARD; PRT; 615 AA.
 AC Q59005; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Hypothetical glycosidic hydrolase MJ1610 (EC 3.2.1.-).
 GN MJ1610.
 OS Methanococcus jannaschii.
 OC Archaea; Buryarchaeota; Methanococcaceae; Methanococci; Methanococcales;
 OC Methanocoldococcaceae; Methanococcaceae;
 OC Methanocoldococcus.
 RN [1]
 RP SSQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE:96331999; PubMed=8888087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Cocayne J.D.,
 RA Kerlavage A.R., Bouherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock G.G., Merrick J.M., Glodkiewicz H.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.",
 RL Science 273:1058-1073(1996)
 CC -- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U67601; AAB99630.1; --.
 DR A64501; A64501.
 DR TIGR; MJ1610; --.
 DR InterPro; IPR000165; Glyco hydro 15.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR InterPro; IPR006465; Oligosaccharyl.
 DR Pfam; PF00723; GLYCO_hydro 15; 1.
 DR PROSITE; PS00820; GLUCOAMYLASE_1.
 DR PROSITE; PS00820; GLUCOAMYLASE_1.
 KW Hypothetical protein; Hydrolase; Glycosidase; Complete proteome.
 FT ACT SITE 406 406 GENERAL_ACID_CATALYST (BY SIMILARITY)
 FT ACT_SITE 407 407 INTERACT WITH SUBSTRATES (BY SIMILARITY).
 FT SEQUENCE 615 AA; 72007 MN; 2B37EB89FP0357BE5 CRC64;

Query Match 8.0%; Score 221.5; DB 1; Length 615;
 Best Local Similarity 23.1%; Pred. No. 2.9e-07;
 Matches 101; Conservative 46; Mismatches 125; Indels 165; Gaps 20;

QY 59 GIVVAPSTDNPDPYFTWTRDSDGLVLUKTULDLFRNGDTSILSTIENYTSQAQATVOQISNP 118
 DB 284 GGIARAPSL-HPDTRIVWGRD-GSYIYSTADLF----GIRNIDRFFEFMSKIQ---- 331
 QY 119 SGDLSGAGIGEPEKFENVDTAYGCSW-----GRPQRDGPAALRATM---TGFGQML 167
 DB 332 -----NAD----GSWLQRYYYVNGKP-----RLTAQTDQIGSILWAM 364
 QY 168 DNGTISTATDIVWPLVRNLDSYVQIWNQTG-----YDLWEENGGSSFF 211
 DB 365 DVHRYLT-----GIRKPVVERYWNTEKAANYLRLVALNTPCPCDLWERFGVFAV 414
 QY 212 TAVOHRALVEASFATAV-----GSSCSMCDSQAPEELCYLQSFWTGSPFLANFD 262
 DB 415 TMGATYAGLKKCAISMSKANRKDKVKGKTIETLKHEWPKRFLYLE-----D 461

QY 253 SSRSGKDNTLGSIHTPDEACDOSTFQSPRALAHKVEUDSPRSIYVNDGSDS 322
 DB 462 EERFAKSINPL-----DKTIDTSILGSYPFNLD---VDDERMIKI-----A 501
 QY 323 EAV-----AVGRPFDTYGNWFLCLILAA---EQYDALYQMDKGSCLEVTV 370
 DB 502 EAIEKAFKYKVSGIGRVEFDIYFGGNPMWITLWLSLYRRILYKVLKEKDDNGA---DI 557
 DT 371 SJDFPKALYSDAATGTWSSSSTYSSIVDAVKTFADGFSVIVETHAASNSMSSEQYKSD 430
 QY 558 YLOKSKKUPNWVKYSF-----DGLFPEQIHKEL 586
 DB 431 GBOLSRDULTWSTAALL 447
 DB 587 GVPMSAMPILGWSNAMFL 603

Search completed: June 17, 2004, 17:46:29
 Job time : 21 secs